

Result No.	Query	Score	Match	Length	DB	ID	Description	
1	387	58.4	228	7	US-60-485-404-49	Sequence 49, Appl		
2	385.5	58.1	118	6	US-10-275-046-68	Sequence 68, Appl		
3	383	57.8	121	6	US-10-275-046-78	Sequence 78, Appl		
4	382	57.6	249	1	PCT-US03-25457-53	Sequence 53, Appl		
5	381	57.5	115	6	US-10-447-331-5	Sequence 5, Appl		
6	381	57.5	313	6	US-10-291-265-427	Sequence 427, App		
7	379.5	57.2	384	6	US-10-291-265-804	Sequence 804, App		
8	379.5	57.2	384	6	US-10-291-285-805	Sequence 805, App		
9	379.5	57.2	384	6	US-10-291-285-806	Sequence 806, App		
10	379.5	57.2	384	6	US-10-291-265-807	Sequence 807, App		
11	378	57.0	113	5	US-09-723-752B-11	Sequence 11, Appl		
12	378	57.0	123	1	PCT-US03-21304-56	Sequence 56, Appl		
13	377.5	56.9	246	6	US-10-602-727-50	Sequence 50, Appl		
14	376	56.7	119	1	PCT-US03-21390-6	Sequence 6, Appl		
15	376	56.7	119	6	US-10-600-152-15	Sequence 15, Appl		
16	376	56.7	119	6	US-10-619-754-6	Sequence 6, Appl		
17	376	56.7	119	6	US-10-608-626-6	Sequence 6, Appl		
18	376	56.7	449	6	US-10-463-442-21	Sequence 21, Appl		
19	375	56.6	244	6	US-10-602-727-51	Sequence 51, Appl		
20	375	56.6	244	6	US-10-602-727-53	Sequence 53, Appl		
21	375	56.6	244	6	US-10-602-727-55	Sequence 55, Appl		
22	373	56.3	244	6	US-10-602-727-56	Sequence 56, Appl		
23	372.5	56.2	238	6	US-10-336-041A-1	Sequence 1, Appl		
24	372.5	56.2	240	6	US-10-336-041A-10	Sequence-10, Appl		
25	372.5	56.2	240	6	US-10-336-041A-12	Sequence 12, Appl		
26	372.5	56.2	241	6	US-10-336-041A-11	Sequence 11, Appl		

QY	2	VTLDES	GGLQ	TPEGG	ALSLVCKA	SAGFTFSSHGMMWVRQT	PKGLEWVAGISNTGYTYYA	61
Db	2	VQLVESGGGLVLP	PGGSURLS	CAASGF	FSSYAMSVWRQAP	KGLEWSAISGSGSTYYA	61	
QY	62	PAYKGRATISR	DNGQSTVRLQ	LNLRAEDTGTYYC	AKGAYCACGGDIDAWGHGEIV	121		
Db	62	DSYGRTFISR	DNKSNTLYQMNSL	RAEDTAVYCARSPMYEG--FDLWGQGLTVT	119			
QY	122	SS	123					
Db	120	SS	121					

	Query Match	57.5%	Score 381;	DB 6;	Length 115;
	Best Local Similarity	61.5%;	Pred. No. 1.6e-23;		
	Matches	75;	Conservative 11;	Mismatches 28;	Indels 8; Gaps 1;
QY	2	VTLDSEGGGGLQTPGGALSLVKASGTTFFSSHGMWVROTQPKGLEWAGISNTGTYYTA	61		
Db	2	VOLOESGGNLPVGGSLRLSCAASGTTFFSSYAMSWVROAPKGLEWVAISGSGGNTYYA	61		



FILE REFERENCE: 21272-017 (785)  
CURRENT APPLICATION NUMBER: US/10/291,265  
CURRENT FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/617,746  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 09/631,451  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 09/633,870  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 944  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 806  
LENGTH: 384  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-291-265-806

Query Match 57.2%; Score 379.5; DB 6; Length 384;  
Best Local Similarity 57.8%; Pred. No. 6.1e-23;  
Matches 78; Conservative 12; Mismatches 32; Indels 13; Gaps 2;  
QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSSHGMMWVRQTPGKLEWAGISNT-GTYTY 60  
DB 21 VOLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSVWRQAPGKLEWVSGLSGSGSSTYY 80  
QY 61 APAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGD----- 109  
DB 81 ADSVKGRFTISRDNKNTLYLQMNLSRADDTARYYCAKGGVELASTKPSIWRLNPIRYW 140  
QY 110 -IDAWGHGTEIVSS 123  
DB 141 YFDLWGQGTTLTVSS 155

RESULT 10  
US-10-291-265-807  
Sequence 807, Application US/10291265  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
FILE REFERENCE: 21272-017 (785)  
CURRENT APPLICATION NUMBER: US/10/291,265  
CURRENT FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/617,746  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 09/631,451  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 09/633,870  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 944  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 807  
LENGTH: 384  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-291-265-807

Query Match 57.2%; Score 379.5; DB 6; Length 384;  
Best Local Similarity 57.8%; Pred. No. 6.1e-23;  
Matches 78; Conservative 12; Mismatches 32; Indels 13; Gaps 2;  
QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSSHGMMWVRQTPGKLEWAGISNT-GTYTY 60  
DB 21 VOLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSVWRQAPGKLEWVSGLSGSGSSTYY 80  
QY 61 APAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGD----- 109  
DB 81 ADSVKGRFTISRDNKNTLYLQMNLSRADDTARYYCAKGGVELASTKPSIWRLNPIRYW 140

QY 110 -IDAWGHGTEIVSS 123  
DB 141 YFDLWGQGTTLTVSS 155  
RESULT 11  
US-09-723-752B-11  
Sequence 11, Application US/09723752B  
GENERAL INFORMATION:  
APPLICANT: Baca, Manuel  
Wells, James A.  
Presta, Leonard G.  
Lowman, Henry B.  
Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,752B  
FILING DATE: 27-Nov-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/908469  
FILING DATE: 06-AUG-1997  
APPLICATION NUMBER: 08/833504  
FILING DATE: 07-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Cui, Steven X.  
REGISTRATION NUMBER: 44,637  
REFERENCE/DOCKET NUMBER: P1093P1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-723-752B-11

Query Match 57.0%; Score 378; DB 5; Length 113;  
Best Local Similarity 62.3%; Pred. No. 2.7e-23;  
Matches 76; Conservative 10; Mismatches 26; Indels 10; Gaps 1;  
QY 2 VTLDSEGGGLQTPGGALSLVKASGFTFSSHGMMWVRQTPGKLEWAGISNTGYTYA 61  
DB 2 VOLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSVWRQAPGKLEWVSGDGGSTYYA 61  
QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGGDIDAWGHGTEIV 121  
DB 62 DSVKGRFTISRDNKNTLYLQMNLSRADDTARYYCARG-----FDYWGQGTTLTV 111  
QY 122 SS 123  
DB 112 SS 113

RESULT 12  
PCT-US03-21304-56  
Sequence 56, Application PC/TUS0321304

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RESULT 13
US-10-602-727-50
; Sequence 50, Application US/10602727
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies Against Protective Antigen
; FILE REFERENCE: PF596PIN
; CURRENT APPLICATION NUMBER: US/10/602,727
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/391,162
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/406,339
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/417,305
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/426,360
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/434,807
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/438,004
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 60/443,858
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/443,781
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/454,613
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/468,651
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PWD0283 scfv

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RESULT 15  
US-10-600-152-15  
; Sequence 15, Application US/10600152  
; GENERAL INFORMATION:  
; APPLICANT: Baughman, Sharon A.  
; APPLICANT: Shak Steven  
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies  
; FILE REFERENCE: P1775R1  
; CURRENT APPLICATION NUMBER: US/10/600,152  
; CURRENT FILING DATE: 2003-06-20

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; PRIOR APPLICATION NUMBER: 09/648,067
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH consensus sequence
US-10-600-152-15
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Query Match      56.7%; Score 376; DB 6; Length 119;
Best Local Similarity 63.4%; Pred. No. 4.1e-23;
Matches 78; Conservative 10; Mismatches 29; Indels 6; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGYTYA 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 VLVESGGGLVOPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAVISGGGTYA 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 62 PAVKGRATISRDNQSTVRLQLNNLRADTGTYCAKGCAYCAGCGDI-DAWGHGTEVI 120
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 DSVKGRFTISRDNKNTLYLQMNLSLRADTAVYYCARGV-----GYSLYDWGQGLVT 116
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 VSS 123
   | | |
Db 117 VSS 119
```

Search completed: September 3, 2003, 12:54:36  
Job time : 9.10781 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:02:54 ; Search time 10.5703 Seconds  
(without alignments)  
1119.054 Million cell updates/sec

Title: US-10-083-424A-18  
Perfect score: 663  
Sequence: 1 AVTLDESGGLQTPGGALSL.....AGCGGDIDANGHGTETVSS 123  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	81.6	585	2 A46507	Ig alpha chain - c
2	522	78.7	138	2 A33334	Ig heavy chain pre
3	475.5	71.7	342	2 A46529	Ig gamma chain (5
4	475.5	71.7	572	2 B46529	Ig y heavy chain (
5	394	59.4	119	2 C36005	Ig heavy chain v r
6	387.5	58.4	141	2 S31669	Ig heavy chain v r
7	386	58.2	123	2 S31114	Ig heavy chain - h
8	385	58.1	140	2 S31686	Ig heavy chain v r
9	383.5	57.8	120	2 S48798	Ig heavy chain v r
10	383	57.8	119	2 S31107	Ig heavy chain - h
11	381	57.5	119	2 S31108	Ig heavy chain - h
12	380.5	57.4	147	2 I37780	Ig variable region
13	380	57.3	146	2 I47196	Ig heavy chain var
14	378	57.0	134	2 S31699	Ig heavy chain v r
15	378	57.0	160	2 S05271	Ig heavy chain pre
16	377	56.9	138	2 S31666	Ig heavy chain v r
17	376	56.7	121	2 S19666	Ig heavy chain v r
18	375.5	56.6	117	2 I47185	Ig heavy chain var
19	375	56.6	145	2 S78486	Ig heavy chain v r
20	375	56.6	121	2 I55673	Ig heavy chain - h
21	372.5	56.2	118	2 S31116	Ig heavy chain - h
22	372.5	56.2	136	2 S31587	Ig heavy chain v r
23	372	56.1	119	2 D36005	Ig heavy chain v r
24	372	56.1	127	2 S38489	Ig heavy chain - h
25	372	56.1	140	2 I47204	Ig heavy chain var
26	371.5	56.0	128	2 S26790	Ig heavy chain v r
27	371.5	56.0	128	2 S26786	Ig heavy chain v r
28	371.5	56.0	145	2 I47203	Ig heavy chain var
29	371	56.0	152	2 B26471	Ig heavy chain pre

30 370 55.8 140 2 S31588 Ig heavy chain v r  
31 369 55.7 117 2 S34012 Ig heavy chain v r  
32 368.5 55.6 120 2 E49590 Ig heavy chain v r  
33 366.5 55.3 124 2 S20782 Ig heavy chain v r  
34 366.5 55.3 140 2 S70442 Ig heavy chain pre  
35 366.5 55.3 145 2 I47186 Ig heavy chain var  
36 366.5 55.3 151 2 A60943 Ig heavy chain pre  
37 366 55.2 120 2 S36278 Ig heavy chain v r  
38 366 55.2 121 2 S26798 Ig heavy chain - h  
39 366 55.2 123 2 S31509 Ig heavy chain v r  
40 366 55.2 132 2 S31603 Ig heavy chain v r  
41 366 55.2 143 2 S23624 Ig heavy chain v r  
42 365.5 55.1 114 2 S31120 Ig heavy chain - h  
43 365.5 55.1 128 2 S48797 Ig heavy chain v r  
44 365.5 55.1 135 2 I37778 Ig variable region  
45 365 55.1 124 2 C27888 Ig heavy chain v r

ALIGNMENTS

RESULT 1  
A46507  
Ig alpha chain - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-Aug-1999  
C:Accession: A46507  
R:Mansikka, A.  
J. Immunol. 149, 855-861, 1992  
A:Title: Chicken IgA H chains. Implications concerning the evolution of H chain gene  
A:Reference number: A46507; MUID:92340889; PMID:1634774  
A:Accession: A46507  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-585 <MAN>  
A:Cross-references: GB:S40610; NID:g251907; PID:g251908  
A:Note: sequence inconsistent with the nucleotide translation  
C:Note: sequence extracted from NCBI backbone (NCBI:109906, NCBIP:109907)  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 541; DB 2; Length 585;  
Best Local Similarity 82.9%; Pred. No. 1.8e-39;  
Matches 102; Conservative 6; Mismatches 15; Indels 0; Gaps 0;  
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVROTCKGLEWAGISNTGTYY 60  
Db 20 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVROTCKGLEWAGISNTGTYY 79  
QY 61 APAYKGRATSRDNGQSTVRLQNLNLAEDTGTYYCAKGGYAGCGGIDANGHGTETVI 120  
Db 80 GPAVQGRATSRDNGQSTVRLQNLNLAEDTGTYYCAKGGYAGCGGIDANGHGTETVI 139  
QY 121 VSS 123  
Db 140 VSS 142

RESULT 2  
A33334  
Ig heavy chain precursor V region - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 20-Dec-1989 #sequence\_revision 20-Dec-1989 #text\_change 21-Jan-2000  
C:Accession: A33334  
R:Reynaud, C.A.; Dahan, A.; Anquez, V.; Weill, J.C.  
Cell 59, 171-183, 1989  
A:Title: Somatic hyperconversion diversifies the single V-H gene of the chicken w  
A:Reference number: A33334; MUID:90003227; PMID:2507167  
A:Accession: A33334  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-138 <REY>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 522; DB 2; Length 138;  
Best Local Similarity 84.6%; Pred. No. 2.1e-38;  
Matches 104; Conservative 2; Mismatches 13; Indels 4; Gaps 1;

QY 1 AVTLDESGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60  
Db AVTLDESGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60  
QY 61 APAVKGRATISRDNGQSTVRLQNLNRAEDTGYTYCAKGGYACGCGGDDAWGHGTEVI 120  
Db GSAVKGRATISRDNGQSTVRLQNLNRAEDTGYTYCAKGGYACGCGGDDAWGHGTEVI 120  
QY 121 VSS 123  
Db 136 VSS 138

## RESULT 3

A46529  
Ig gamma chain (5.7S) - duck (fragment)  
C;Species: Anas platyrhynchos (domestic duck)  
C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C;Accession: A46529; S20760  
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.  
J. Immunol. 149, 2627-2633, 1992  
A;Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos: m  
A;Reference number: A46529; MUID:93017865; PMID:1401901  
A;Accession: A46529  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-342 <MAG>

A;Cross-references: EMBL:X65218; NID:962444; PIDN:CAA46321.1; PID:g1334619  
A;Experimental source: spleen  
A;Note: sequence extracted from NCBI backbone (NCBIP:116122)  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;22-104/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 475.5; DB 2; Length 342;  
Best Local Similarity 74.8%; Pred. No. 5.3e-34;  
Matches 95; Conservative 10; Mismatches 17; Indels 5; Gaps 3;  
QY 1 AVTLDESGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60  
Db 8 AETLDESGGLVSPGSLTLVCKSGFTFSSNEMVVRQAPGKLEWVAGIT-TGYTYG 66  
QY 61 APAVKGRATISRDNGQSTVRLQNLNRAEDTGYTYCAK--GGAYCA--CGCGDIDAWGHG 116  
Db 67 APAVKGRATISRDNGQSTVRLQNLNRAEDTGYTYCAKTTGYANCAGYCAADIDLWGHG 126  
QY 117 TEVIVSS 123  
Db 127 TEVIVSS 133

## RESULT 4

B46529  
Ig y heavy chain (7.8S) - duck  
N;Alternate names: Ig gamma chain (7.8S)  
C;Species: Anas platyrhynchos (domestic duck)  
C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C;Accession: B46529; S20759  
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.  
J. Immunol. 149, 2627-2633, 1992  
A;Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos: m  
A;Reference number: A46529; MUID:93017865; PMID:1401901  
A;Accession: B46529  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-572 <MAG>

A;Cross-references: EMBL:X65219; NID:962442; PIDN:CAA46322.1; PID:g62443  
A;Experimental source: spleen  
A;Note: sequence extracted from NCBI backbone (NCBIP:116127)  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;37-120/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 475.5; DB 2; Length 572;  
Best Local Similarity 74.0%; Pred. No. 8.6e-34;  
Matches 91; Conservative 12; Mismatches 19; Indels 1; Gaps 1;  
QY 1 AVTLDESGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTY 60  
Db 23 AATLDESGGLVSPGSLTLVCKSGFTFSSYGVSVVRQAPGKLEWVAGITDSGGSTYY 82  
QY 61 APAVKGRATISRDNGQSTVRLQNLNRAEDTGYTYCAKGGYACGCGGDDAWGHGTEVI 120  
Db 83 APAVKGRATISRDNGQSTVRLQNLNRAEDTGYTYCAKGGYACGCGGDDAWGHGTEVI 120  
QY 121 VSS 123  
Db 142 VSS 144

## RESULT 5

C36005  
Ig heavy chain V region (30pl) - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Aug-1996  
C;Accession: C36005  
R;Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable  
A;Reference number: A36005; MUID:90349571; PMID:2117273  
A;Accession: C36005  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-119 <SCH>

A;Cross-references: GB:M18513  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.4%; Score 394; DB 2; Length 119;  
Best Local Similarity 64.8%; Pred. No. 2.3e-27;  
Matches 79; Conservative 10; Mismatches 29; Indels 4; Gaps 1;  
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGTYTYA 61  
Db 2 VOLLDSEGGGLVSPGSLTLVCKSGFTFSSYCAASGFTFSSYMSVVRQAPGKLEWVSAISGSGSTYYA 61  
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTYCAKGGYACGCGGDDAWGHGTEVI 121  
Db 62 DSVKGRATISRDNGQSTVRLQNLNRAEDTGYTYCAKGGYACGCGGDDAWGHGTEVI 121  
QY 122 SS 123  
Db 118 SS 119

## RESULT 6

S31669  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31669  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.  
Submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t  
A;Reference number: S31585  
A;Accession: S31669  
A;Status: preliminary  
A;Molecule type: mRNA





\*\*\*\*\*

Search completed: September 3, 2003, 12:16:29  
Job time : 10.5703 secs

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RESULT 2  
HV3K\_HUMAN  
ID HV3K HUMAN  
STANDARD: PRT: 126 AA.

AC P01772;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region KOL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE AND DISULFIDE BONDS.  
 RX MEDLINE=83289131; PubMed=6884994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
 RT "Three-dimensional structure determination of antibodies. Primary  
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.",  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=81072295; PubMed=7441755;  
 RA Marquart M., Deisenhofer J., Huber R., Palm W.;  
 RT "Crystallographic refinement and atomic models of the intact  
 immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A  
 and 1.0-A resolution".  
 RL J. Mol. Biol. 141:369-391(1980).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02055; GIHUKL.  
 DR PDB; 2FB4; 12-JUL-89.  
 DR PDB; 2IG2; 12-JUL-89.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.  
 KW DOMAIN 1 112 IG-LIKE.  
 FT MOD\_RES 1 112  
 FT DISULFID 22 96  
 FT DISULFID 105 110  
 FT STRAND 3 7  
 FT STRAND 11 12  
 FT TURN 14 15  
 FT STRAND 18 25  
 FT STRAND 29 31  
 FT STRAND 34 39  
 FT TURN 41 42  
 FT STRAND 45 51  
 FT TURN 53 54  
 FT STRAND 58 60  
 FT STRAND 62 64  
 FT STRAND 65 65  
 FT TURN 66 67  
 FT STRAND 68 73  
 FT TURN 74 77  
 FT STRAND 78 83  
 FT HELIX 88 90  
 FT STRAND 92 99  
 FT STRAND 106 106  
 FT TURN 107 108  
 FT STRAND 109 109  
 FT STRAND 113 116  
 FT STRAND 120 124  
 FT NON\_TER 126 126  
 SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;  
 Query Match 52.4%; Score 347.5; DB 1; Length 126;  
 Best Local Similarity 57.1%; Pred. No. 3.3e-26;  
 Matches 72; Conservative 17; Mismatches 32; Indels 5; Gaps 3;  
 QY 2 VTLDSEGGGLQTPGGALSVCASGFTFSSHGMMWVROTPGKLEWVAGISNTGTYTYA 61

Db 2 VOLVESGGGVQPGSLRLSCSSSGFTFSSYAMVWRQAPGKLEWVAILWDDGSDQHYA 61  
 QY 62 PAVKGRATISRNGQSTVRLQLNLRADTGTYYCAKGG--AYC--AGCGDDIDANGHGT 117  
 Db 62 DSVKGRFTISRDNKNTLFQMDSLRPEDTGVYFCARDGSGHGFCSASCFCGP-DYWGQGT 120  
 QY 118 EVIVSS 123  
 Db 121 PVTIVSS 126  
 RESULT 3  
 HV3C\_HUMAN STANDARD; PRT; 117 AA.  
 ID P01764;  
 AC P01764;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region VH26 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81101090; PubMed=6450418;  
 RA Matthysens G., Rabbitts T.H.;  
 RT "Structure and multiplicity of genes for the human immunoglobulin  
 heavy chain variable region".  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation.  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; J00236; AA53516.1; -.  
 DR EMBL; M35415; AA58735.1; -.  
 DR PIR; A02047; H3HU26.  
 DR PDB; 1HOU; 23-DEC-99.  
 DR Genes; HGNC:5545; IGHV6.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal; 3D-structure.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.  
 FT DOMAIN 20 >117 IG-LIKE.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;  
 Query Match 52.2%; Score 346; DB 1; Length 117;  
 Best Local Similarity 68.0%; Pred. No. 4.2e-26;  
 Matches 66; Conservative 10; Mismatches 21; Indels 0; Gaps 0;  
 QY 2 VTLDSEGGGLQTPGGALSVCASGFTFSSHGMMWVROTPGKLEWVAGISNTGTYTYA 61  
 Db 21 VOLVESGGGLVQPGSLRLSCASGFTFSSYAMVWRQAPGKLEWVSAISGSGGTYTG 80  
 QY 62 PAVKGRATISRNGQSTVRLQLNLRADTGTYYCAK 98  
 Db 81 DSVKGRFTISRDNKNTLYLQMSLRADTAVYYCAK 117

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Db          135 SS 136

RESULT 5
HV35_MOUSE
ID HV35_MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region HPC76 (Fragment).
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81013937; PubMed=6251474;
RR Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
RT between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
CC REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CC CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02074; MMSV76.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT NON_TER 1
FT DOMAIN <1 110
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;

Query Match 51.7%; Score 342.5; DB 1; Length 111;
Best Local Similarity 58.8%; Pred. No. 8.6e-26;
Matches 70; Conservative 14; Mismatches 26; Indels 9; Gaps

QY 6 ESGGGLTPGALSLVCASGTFSSHGMMWVROTQPKGLEWAGIS-NTGTYTYAPAV 64
DB 1 ESGGGLVQPGSGMKLSCVASGTFFSNYMNNWVQSPKGLEWVAEIRLKSGYATHYAESV 60
QY 65 KGRATISRDNGQSVRLQLNLRADTGTGYTCAGKAYCAGCGGDDAWHGTEVIYSS 123
DB 61 KGRFTISRDSKSSVYLQMNLRADTGIYCTRPCV-----PDYWGQGTTLTVSS 111

RESULT 6
HV27_MOUSE
ID HV27_MOUSE STANDARD; PRT; 113 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region A4.
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RR Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

```

Query Match	51.4%;	Score 340.5;	DB 1;	Length 122;	
Best Local Similarity	57.1%;	Pred. No. 1.5e-25;			
Matches	72;	Conservative 13;	Mismatches 32;	Indels 9;	Gaps

QY	2	VTLDESGGGGLTPGCAISLVCKASGFTFSSHGMMWVROT	PKGKLEWVAGISNTGTYTYA	61
DB	2	VELYESGGVVZPKRSURLSCAASGFTFSNTAMHWMVROP	PKGKLEWVAISYBGBBKYYA	61
QY	62	PAVKGRTATISRDNGQSTVRLQNNLRAEDTGYTYCAKG	-----GAYCAGCGGSDIDAWGHGT	117
DB	62	BSVKGRTISRDSBKBTLYLQNNSLRAEBTAVYICARDEP	LYGBYRA-----FNWGGQT	116
QY	118	EVIVSS	123	
DB	117	LTVSS	122	

RESULT 8

HV28_MOUSE	STANDARD;	PRT;	113 AA.
ID	HV28_MOUSE		
AC	P01797;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	13-SEP-2003 (Rel. 42, Last annotation update)		
DE	Ig heavy chain V-III region U61.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;			
FN	[1]		
SEQUENCE.			
RY	MEDLINE=78158406; PubMed=417344;		
RX	Vrana M., Rudikoff S., Potter M.;		
RT	"Sequence variation among heavy chains from inulin-binding myeloma		
RT	proteins.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).		
CC	-I- MISCCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT		
CC	BINDS INULIN.		
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.		
DR	PIR: B93818; AVMS61.		
DR	HSP; P01810; 2FEJ.		
DR	InterPro: IPR007110; Ig-like.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_v.		
DR	Pfam: PF00047; Ig. 1.		
DR	SMART: SM00406; IGV. 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	Immunoglobulin V region.		
FT	DOMAIN 1 >113		
FT	DISULFID. 22 98		
FT	NON_TER. 113: 113		
SQ	SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;		

Query Match

51.3%;	Score 340;	DB 1;	Length 113;		
Best Local Similarity	58.2%;	Pred. No. 1.5e-25;			
Matches	71;	Conservative 13;	Mismatches 26;	Indels 12;	Gaps 2;

QY	2	VTLDESGGGGLTPGCAISLVCKASGFTFSSHGMMWVROT	PKGKLEWVAGI--SNTGTYTY	59
DB	2	VKLEESGGGLVQPGGSKLSCVSGFTFSNYMMWVROSPEK	GLEWVAEIRLKSNIYATH	61
QY	60	YAPAVKGRATISRDNGQSTVRLQNNLRAEDTGYTYCAKG	GAYCAGCGGSDIDAWGHGT	119
DB	62	YAEVKGRTISRDSKSSVLYQNNLRAEDTGYTYCTG	FAY-----WGQGLV	111
QY	120	IV	121	
DB	112	IV	113	

RESULT 9

HV33_MOUSE	STANDARD;	PRT;	115 AA.
ID	HV33_MOUSE		



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AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA JOHNSON N., Slankard J., Paul L., Hoob L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
      BINDS INULIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; D92811; AVMS82.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 984517648C121C5A CRC64;

Query Match 51.0%; Score 338; DB 1; Length 115;
Best Local Similarity 56.5%; Pred. No. 2.4e-25;
Matches 70; Conservative 15; Mismatches 27; Indels 12; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLWVAGI--SNTGTYTY 59
   I:||||| I::: I:|||||: I:|||||: I:|||||: I:
Db 2 VKLEESGGGLVQPGGSKLSCVASGFTFSNWMNVRSPEKGLWVAEIRLKSHNYATH 61
   I:||||| I::: I:|||||: I:|||||: I:|||||: I:

QY 60 YAPAVKGRATISRDNGQSTVRLQLNNRAEDTGYTCAGKAYCAGCGGDDIADWGHGTEV 119
   I:||||| I::: I:|||||: I:|||||: I:|||||: I:
Db 62 YAESVKGRTISRDKSSVYLRNNLRPEDTGYICTTGFPAY-----WGQGTLLV 111
   I:||||| I::: I:|||||: I:|||||: I:|||||: I:

QY 120 IVSS 123
Db 112 TVSA 115

RESULT 10
ID HV02_CANFA STANDARD; PRT; 117 AA.
AC P01785;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOO.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 1-112.
RX MEDLINE=77242268; PubMed=407924;
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
immunoglobulin heavy chains."
RL Biochemistry 16:3160-3168(1977).
RN [2]
RP SEQUENCE OF 113-117.
RX MEDLINE=80077682; PubMed=1117299;
RA McCumber L.J., Capra J.D.;

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RT "The complete amino-acid sequence of a canine mu chain.";
RL Mol. Immunol. 16:565-570(1979).
CC -|- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90403; MHDGMO.
DR HSP; P01772; 2FBA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 51.0%; Score 338; DB 1; Length 117;
Best Local Similarity 58.4%; Pred. No. 2.4e-25;
Matches 73; Conservative 14; Mismatches 26; Indels 12; Gaps 3;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYTYA 61
   I:||||| I::: I:|||||: I:|||||: I:|||||: I:
Db 2 VKLVESGGDLVKPGGSLRSLSCVASGFTFSSNGSMVVRQDPGGLQWVADISSG-QTYYA 60
   I:||||| I::: I:|||||: I:|||||: I:|||||: I:

QY 62 PAVKGRATISRDNGQSTVRLQLNNRAEDTGYTCAGKAYCAGCGGDDIDA---WGHGTE 118
   I:||||| I::: I:|||||: I:|||||: I:|||||: I:
Db 61 DAVKGRFSISRDNARNTLYQMEDLRVEDTAVIYCA-----TEGDIEIPRFGQGTI 112
   I:||||| I::: I:|||||: I:|||||: I:|||||: I:

QY 119 VIVS 123
Db 113 VTSS 117

RESULT 11
ID HV30_MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
protein."
RL Biochemistry 16:1170-1175(1977).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
      BINDS INULIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90400; AVMSB7.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 50.8%; Score 337; DB 1; Length 113;
Best Local Similarity 57.4%; Pred. No. 2.9e-25;
Matches 70; Conservative 14; Mismatches 26; Indels 12; Gaps 2;

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QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTQPKGLEWVAGI--SNTGTITY 59  
 Db 2 VKLEESGGGLVQPGGSMKLSVASGFTFSNWMVRSPEKLEWVAEIRLKSHTYATH 61  
 QY 60 YAPAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAGKAYCAGCGGIDAWGHGTEV 119  
 Db 62 YAESVKGRTISRDKSSVYLQMNLRADTAIYCGTGFAF-----WGQGLTV 111  
 QY 120 IV 121  
 Db 112 TV 113

## RESULT 12

HV3B\_HUMAN  
 ID HV3B\_HUMAN STANDARD; PRT; 114 AA.  
 AC P01763;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 OS Ig heavy chain V-III region WEA.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RA MEDLINE=83273707; PubMed=6410398;  
 RA Goni F., Frangione B.;  
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
 RT galactose in Klebsiella polysaccharides K30 and K33.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
 CC WALDENSTROM'S MACROGLOBULINEMIA.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02046; M3HWE.  
 DR HSSP; P01772; 2PB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT MOD\_RES 1 112 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

## Query Match

Best Local Similarity 50.6%; Score 335.5; DB 1; Length 114;  
 Matches 66; Conservative 20; Mismatches 27; Indels 9; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTQPKGLEWVAGISNTGTITYA 61  
 Db 2 VOLVDSGGGLVEPGGSLRLSCASGFTFSNDMMVRSQAPKGLWLSFISGGSTIYA 61  
 QY 62 PAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAGKAYCAGCGGIDAWGHGTEV 121  
 Db 62 DSVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAGKAYCAGCGGIDAWGHGTEV 121  
 QY 122 SS 123  
 Db 113 SS 114

## RESULT 13

HV29\_MOUSE  
 ID HV29\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01798;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 OS Ig heavy chain V-III region EI09.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=78158406; PubMed=417344;  
 RA Vrana M., Rudikoff S., Potter M.;  
 RT "Sequence variation among heavy chains from inulin-binding myeloma  
 RT proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 CC BINDS INULIN.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; C93818; AVMS09.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 >113 IG-LIKE.  
 FT DISULFID 22 98  
 FT NON\_TER 113 113 BY SIMILARITY.  
 SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;

## Query Match

Best Local Similarity 50.5%; Score 335; DB 1; Length 113;  
 Matches 69; Conservative 15; Mismatches 26; Indels 12; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTQPKGLEWVAGI--SNTGTITY 59  
 Db 2 VKLEESGGGLVQPGGSMKLSVASGFTFSNWMVRSQAPKGLWLSFISGGSTIYA 61  
 QY 60 YAPAVKGRATISRDNQSTVRLQNLNRAEDTGTYYCAGKAYCAGCGGIDAWGHGTEV 119  
 Db 62 YAESVKGRTISRDKSSVYLQMNLRADTAIYCGTGFAF-----WGQGLTV 111  
 QY 120 IV 121  
 Db 112 TV 113

## RESULT 14

HV3H\_HUMAN  
 ID HV3H\_HUMAN STANDARD; PRT; 122 AA.  
 AC P01769;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 OS Ig heavy chain V-III region GA.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=74175307; PubMed=4208843;  
 RA Florent G., Lehman D., Putnam F.W.;  
 RT "The switch point in mu heavy chains of human IgM immunoglobulins.";  
 RL Biochemistry 13:2482-2498(1974).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02052; M3HUGA.  
DR HSP; P01772; 2FB4.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 112 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 50.3%; Score 333.5; DB 1; Length 122;  
Best Local Similarity 52.5%; Pred. No. 6.7e-25;  
Matches 64; Conservative 19; Mismatches 38; Indels 1; Gaps 1;  
QY 2 VTLDSEGGGLQTPGGALSILVKASGTFSSHGMWVRQTPCKGLEWVAGISNTGTYYA 61  
DB 2 VZLVZSGGAVZPGRSLRUSCAASGFSFYAMHWVRQAPGKGLZWLVSIVYGBBZYA 61  
QY 62 YAPVKGRATISRDNQSQTVRLQLNNLRAEDTGTYYCAKGGAYCAGCGDIDAWHGTEV 121  
DB 62 ASVKGRTISRBBKTMYLEMNSLRANTAVYCARSGIALGVSAG-TDYWGZGLTYI 120  
QY 122 SS 123  
DB 121 SS 122

RESULT 15  
ID HV31\_MOUSE STANDARD; PRT; 113 AA.  
AC P01800;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region T957.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81216632; PubMed=6787122;  
RA Rudikoff S., Potter M.;  
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:  
RT evidence for a new heavy chain joining segment.";  
RL J. Immunol. 127:191-194(1981).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS INULIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A92810; AVMS57.  
DR HSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 >113 IG-LIKE.  
FT DISULFID 22 98 BY SIMILARITY.  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Query Match 50.2%; Score 333; DB 1; Length 113;  
Best Local Similarity 57.4%; Pred. No. 6.9e-25;  
Matches 70; Conservative 13; Mismatches 27; Indels 12; Gaps 2;

QY 2 VTLDSEGGGLQTPGGALSILVKASGTFSSHGMWVRQTPCKGLEWVAGI--SNTGTVTV 59  
DB 2 VKLEESGGGLVQPGGSMKLSVCVASGTFFSNYWNVWVRQSPKGLEWVAEIRLKSHNYETH 61  
QY 60 YAPVKGRATISRDNQSQTVRLQLNNLRAEDTGTYYCAKGGAYCAGCGDIDAWHGTEV 119  
DB 62 YAESVKGRFTISRDDSKSSVYLQMNILRAEDTGTYYCTTGFAV-----WGQGTLV 111  
QY 120 IV 121  
DB 112 TV 113

Search completed: September 3, 2003, 12:10:16  
Job time : 5.65885 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	373	56.3	113	4	Q9UL90	Q9UL90 homo sapien
2	372	56.1	597	4	Q96BB9	Q96BB9 homo sapien
3	368.5	55.6	147	4	Q9Y509	Q9Y509 homo sapien
4	365	55.1	119	11	Q9Z0E7	Q9Z0E7 mus musculus
5	364.5	55.0	471	4	Q8TC77	Q8TC77 homo sapien
6	363.5	54.8	118	4	Q9UL91	Q9UL91 homo sapien
7	363.5	54.8	613	4	Q8WUK1	Q8WUK1 homo sapien
8	363	54.8	116	4	Q9UL93	Q9UL93 homo sapien
9	359	54.1	121	4	Q9UL71	Q9UL71 homo sapien
10	357.5	53.9	487	11	Q99KA4	Q99KA4 mus musculus
11	352.5	53.2	494	4	Q96K68	Q96K68 homo sapien
12	351.5	53.0	122	4	Q9UL84	Q9UL84 homo sapien
13	349	52.6	479	11	Q9LWP5	Q9LWP5 mus musculus
14	349	52.6	499	4	Q8N5K4	Q8N5K4 homo sapien
15	348.5	52.6	573	4	Q8WU38	Q8WU38 homo sapien
16	341	51.4	480	11	Q91XE1	Q91XE1 mus musculus

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Db 2 VOLVESGGVQVPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLVWFAFIRYDGSNKYYA 61
QY 62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTTCYCAKGGAYCAGCGGDDIDAWHGTEV 121
Db 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVTYICAK-----DLNHWGGTTLTV 111
QY 122 SS 123
Db 112 SS 113

RESULT 2
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015760; AAH15760.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
Query Match 56.1%; Score 372; DB 4; Length 597;
Best Local Similarity 62.1%; Pred. No. 1.5e-27;
Matches 77; Conservative 11; Mismatches 34; Indels 2; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSHGMMWVRQTPGKGLVWAGISNTGTYTYA 61
Db 21 VOLVESGGVQVPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLVWFAFIRYDGSNKYYA 80
QY 62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTTCYCAKGGAYCAGCGGDDIDAWHGTEV 119
Db 81 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVTYICAKDPRGYSASGNTYREDYWGQGTIV 140
QY 120 IVSS 123
Db 141 TVSS 144

RESULT 3
Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE VH3 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
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RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;
Query Match 55.8%; Score 368.5; DB 4; Length 147;
Best Local Similarity 60.0%; Pred. No. 6.2e-28;
Matches 75; Conservative 13; Mismatches 34; Indels 3; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSHGMMWVRQTPGKGLVWAGISNTGTYTYA 61
Db 2 VHLVESGGVQVPGKSLRLSCAASGFTFSYGMWVRQAPGKGLDWWALLSYDGSSTYYA 61
QY 62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTTCYCAKGGAYCAGCG---GDIDAWHGTE 118
Db 62 GSVKGRFTISRDNKNTLYLQMSLRAEDTAVTYICAKDGNVFDVSGYYAGIDYWGQGT 121
QY 119 VISS 123
Db 122 TVSS 126

RESULT 4
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ackin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307937; AAL09421.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;
Query Match 55.1%; Score 365; DB 11; Length 119;
Best Local Similarity 59.8%; Pred. No. 1e-27;
Matches 73; Conservative 15; Mismatches 30; Indels 4; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSHGMMWVRQTPGKGLVWAGISNTGTYTYA 61
Db 2 VOLVESGGDLVKPGSKLSCAASGFTFSYGMWVRQTPDKRLVWATISSGSGTYTP 61
QY 62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTTCYCAKGGAYCAGCGGDDIDAWHGTEV 121
Db 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVTYICAKHGDDYDVG---FAIWGGTTLTV 117
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QY 122 SS 123
Db 118 SA 119

RESULT 5
Q8TC77
ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC024289; AAH24289.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 55.0%; Score 364.5; DB 4; Length 471;
Best Local Similarity 55.7%; Pred. No. 6.1e-27;
Matches 73; Conservative 16; Mismatches 23; Indels 19; Gaps 2;

QY 2 VTLDESGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKGLEWVAGISNTGTYTYA 61
Db 1 VTLDESGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKGLEWVAGISNTGTYTYA 61
21 VLVESGGGLVPGGSLRLSCAASGFTFSYNNWVRQAPGKGLEWVAVISYDGSNKYYA 80
62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTYYCAKGAYCAGCGGDI-----DA 112
81 DSVKGRFTISRDNKNSLYLQMSLRRAEDTAVYYCAR-----DLRQLTSYWFYDL 130
113 WGHGTEVIVSS 123
131 WGRGTLTVVSS 141

RESULT 6
Q9UL91
ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -

DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 54.8%; Score 363.5; DB 4; Length 118;
Best Local Similarity 61.2%; Pred. No. 1.4e-27;
Matches 74; Conservative 13; Mismatches 29; Indels 5; Gaps 1;

QY 2 VTLDESGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKGLEWVAGISNTGTYTYA 61
Db 2 VLVESGGGLVPGGSLRLSCAASGFTFSYNNWVRQAPGKGLEWVAVISYDGSNKYYA 80
62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTYYCAKGAYCAGCGGDIIDAWGHGTEVIV 121
62 DSVKGRFTISRDNKNSLYLQMSLRRAEDTAVYYCARGDSSEA-----FDIWGQGTMTV 116
122 S 122
117 S 117

RESULT 7
Q8WUK1
ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 54.8%; Score 363.5; DB 4; Length 613;
Best Local Similarity 62.3%; Pred. No. 1e-26;
Matches 76; Conservative 11; Mismatches 32; Indels 3; Gaps 2;

QY 2 VTLDESGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKGLEWVAGISNTGTYTYA 61
Db 21 VLVESGGGVQVGRSLRLSCAASGFTFSYGHVWVRQAPGKGLEWVAVISYDGSNKYYA 80
62 PAVKGRATISRDNGQSTVRLQLNNLRAEDTGTYYCAKGAYCAGCGGDIIDAWGHGTEVIV 121
81 DSVKGRFTISRDNKNSLYLQMSLRRAEDTAVYYCARD--WSEGV-ETFDIWGQGTMTV 137
122 SS 123
117 S 117
138 SS 139
```

## RESULT 8

Q9UL93 ID Q9UL93 PRELIMINARY; PRT; 116 AA.  
AC Q9UL93;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
DE Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035021; AAD56257.1;  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 116  
FT NON\_TER 116  
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 54.8%; Score 363; DB 4; Length 116;  
Best Local Similarity 61.5%; Pred. No. 1.6e-27;  
Matches 75; Conservative 11; Mismatches 30; Indels 6; Gaps 1;  
QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSHGMMVVRQTPGKGLWVAGISNTGYTYA 61  
Db 1 VOLVESGGGVQPGSLRLSCAASGFTFSYAMHWVRQAPGKGLWVAVISYDGSNKYYA 60  
QY 62 PAVKGRATISRDNGSTVRLQLNNLRAEDTGYTYCAKGAYCAGCGGDDIDANGHGTETV 121  
Db 61 DSVKGRFTISRDNKNTLYLQNSLRRAEDTAMYYCAGG-----GLGLGYWGQGLTV 114  
QY 122 SS 123  
Db 115 SS 116

## RESULT 9

Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.  
AC Q9UL71;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
DE Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035043; AAD56279.1;  
DR HSSP; P01772; 2FB4.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 121  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;  
Query Match 54.1%; Score 359; DB 4; Length 121;  
Best Local Similarity 59.8%; Pred. No. 4e-27;  
Matches 73; Conservative 11; Mismatches 36; Indels 2; Gaps 1;  
QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSHGMMVVRQTPGKGLWVAGISNTGYTYA 61  
Db 2 VOLVESGGGVQPGSLRLSCAASGFTFDGYAMHWVRQAPGKGLWVSLISDGGSTYYA 61  
QY 62 PAVKGRATISRDNGSTVRLQLNNLRAEDTGYTYCAKGAYCAGCGGDDIDANGHGTETV 121  
Db 62 DSVKGRFTISRDNKNTLYLQNSLRRAEDTALYYCAKGV--TTIYDRFDINGQGTMTV 119  
QY 122 SS 123  
Db 120 SS 121

## RESULT 10

Q99KA4 ID Q99KA4 PRELIMINARY; PRT; 487 AA.  
AC Q99KA4;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical 52.6 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC004786; AA04786.1;  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 53.9%; Score 357.5; DB 11; Length 487;  
Best Local Similarity 58.9%; Pred. No. 3e-26;  
Matches 73; Conservative 15; Mismatches 33; Indels 3; Gaps 2;  
QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSHGMMVVRQTPGKGLWVAGISNTGYTYA 61  
Db 21 VOLVESGGGLVPGSLRLSCAASGFTFSYAMSWVRQTPKRLWVATISDGSSTYYTP 80  
QY 62 PAVKGRATISRDNGSTVRLQLNNLRAEDTGYTYCAK--GGAYCAGCGGDDIDANGHGTETV 119  
Db 81 DNVKGRFTISRDNKNTLYLQNSLRRAEDTAMYYCARDMGSPYGGY--SRFDYWGQGTI 139  
QY 120 IVSS 123  
Db 140 TVSS 143  
RESULT 11



Q96K68  
ID Q96K68 PRELIMINARY; PRT; 494 AA.  
AC Q96K68;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein FLJ14473.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagatsuma M., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Ninomiya K., Iwavanagi T.;  
RT "NEDO human cDNA sequencing project.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK027379; BAB55072.1; -  
DR InterPro; IPR007110; Ig\_LIKE.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AE4C0E CRC64;  
  
Query Match 53.2%; Score 352.5; DB 4; Length 494;  
Best Local Similarity 56.0%; Pred. No. 9.3e-25;  
Matches 70; Conservative 15; Mismatches 33; Indels 7; Gaps 2;  
  
QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSHGMMWVROTTPGKGLEWVAGISNTGTYTYA 61  
Db 21 VQLVESGGGLVPGGSLRSLSCAASGLSFSTYANNWVRQAPGKGLEWSSISRSYIYR 80  
  
QY 62 PAVKGRATISRDNQSTVRLQLNLRADDTGTYTCAR---GGAYCAGCGGDIADWGHGTE 118  
Db 81 DSVKGRFTISRDNKNSLYLQMSLRVDDTAVTYTCARDCSCNGAICYG----FSPWGQGT 136  
  
QY 119 VIVSS 123  
Db 137 VTVSS 141  
  
RESULT 12  
Q9UL84  
ID Q9UL84 PRELIMINARY; PRT; 122 AA.  
AC Q9UL84;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-98277139; PubMed-9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035030; AAD56266.1; -

DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig\_LIKE.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 122  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;  
  
Query Match 53.0%; Score 351.5; DB 4; Length 122;  
Best Local Similarity 57.0%; Pred. No. 2.1e-26;  
Matches 73; Conservative 12; Mismatches 30; Indels 13; Gaps 2;  
  
QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSHGMMWVROTTPGKGLEWVAGISNTGTYTYA 61  
Db 2 VQLVESGGGVQPGSLRSLSCAASRFTFSNYGMHVRQAPGKGLEWVAALISNDGSKFYA 61  
  
QY 62 PAVKGRATISRDNQSTVRLQLNLRADDTGTYTCAR-----GAYCAGCGGDIADWGH 115  
Db 62 DSVKGRFTISRDNKNSLYLQMSLRVDDTAVTYTCARDCRGLVGY-----FDWQ 114  
  
QY 116 GTEVIVSS 123  
Db 115 GTLVTVSS 122  
  
RESULT 13  
Q91WP5  
ID Q91WP5 PRELIMINARY; PRT; 479 AA.  
AC Q91WP5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 51.6 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC013656; AAH13656.1; -  
DR InterPro; IPR007110; Ig\_LIKE.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;  
  
Query Match 52.6%; Score 349; DB 11; Length 479;  
Best Local Similarity 55.7%; Pred. No. 1.9e-25;  
Matches 68; Conservative 17; Mismatches 29; Indels 8; Gaps 1;  
  
QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSHGMMWVROTTPGKGLEWVAGISNTGTYTYA 61  
Db 21 VQLVESGGGLVPGGSLKVSACAASGLTFSNYAMSVRQSPKRLKLEWVAALISNDGSKFYA 80  
  
QY 62 PAVKGRATISRDNQSTVRLQLNLRADDTGTYTCARGGAYCAGCGGDIADWGHGTEVIV 121  
Db 81 DTMKGRFTISRDNKNSLYLQMSLRSEDTAFYTCVRCGGYF-----DVMGAGTAVTV 132  
  
QY 122 SS 123  
Db 133 SS 134

Q8WU38	PRELIMINARY;	PRT;	573 AA.
ID	Q8WU38		
AC	Q8WU38;		
DT	01-MAR-2002 (TReMBLrel. 20, Created)		
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)		
DE	Hypothetical protein.		
DE	OS Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Tonsil;		
RC	Strasbourg R.;		
RA	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: BC021276; AAH21276.1;		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_V.		
DR	Pfam; PF000047; Ig; 4.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 2.		

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run On: September 3, 2003, 12:00:29 ; Search time 35.9514 Seconds  
(without alignments)  
547.464 Million cell updates/sec

Title: US-10-083-424a-20  
Perfect score: 650  
Sequence: 1 AVTLESGGLTPGALS.....RGSTGIDAWHGTEIVSS 124

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	507.5	78.1	146	19 AAW60170	Chicken Mab heavy
2	499	76.8	145	19 AAW60171	Heavy chain variab
3	491.5	75.6	129	22 AAG78977	Chicken protein #1
4	491	75.5	147	19 AAW60173	Heavy chain variab
5	471	72.5	141	19 AAW60172	Heavy chain variab
6	469.5	72.2	269	21 AAV71010	Chicken phospholam
7	402	61.8	96	23 ABG60417	Selective targetin
8	392	60.3	124	22 AAE07018	Human heavy chain
9	389.5	59.9	384	22 AAM24101	Human EST encoded

10	388	59.7	132	23 ABG69154	Human monoclonal a
11	385	59.2	177	24 AB336939	Anti-CD40 monoclon
12	384	59.1	132	23 ABG69150	Human monoclonal a
13	383	58.9	252	23 ABP45508	Human BlyS binding
14	382	58.8	247	23 ABP44985	Human BlyS binding
15	381.5	58.7	115	21 AAB39519	Anti-IL12 antibody
16	381	58.6	131	22 AAG65566	Amino acid sequenc
17	380.5	58.5	121	23 ABG76929	Humanised antibody
18	380.5	58.5	159	22 AAU14226	Human novel protei
19	380	58.5	126	23 ABG69155	Human monoclonal a
20	379.5	58.4	119	23 AAE28151	Human consensus he
21	379	58.3	122	14 AAR30773	Consensus humanise
22	379	58.3	125	22 AAB62746	Human HIV-1 monocl
23	379	58.3	132	22 AAU00576	VH ligand-binding
24	379	58.3	132	22 AAU00581	Modified VH ligand
25	379	58.3	132	22 AAU00584	Modified VH ligand
26	379	58.3	132	23 ABG69149	Human monoclonal a
27	379	58.3	132	23 ABG69152	Human monoclonal a
28	379	58.3	140	18 AAM13524	Anti-melanoma anti
29	379	58.3	247	23 ABP45319	Human BlyS binding
30	378.5	58.2	117	22 AAE12061	Human anti-tissue
31	378.5	58.2	123	18 AAM08582	Human antibody C4.
32	378.5	58.2	248	23 ABP45865	Human BlyS binding
33	378.5	58.2	313	22 AAU14320	Human novel protei
34	378	58.2	239	23 ABP45911	Human BlyS binding
35	378	58.2	243	23 ABP45924	Human BlyS binding
36	378	58.2	252	23 ABP45190	Human BlyS binding
37	377.5	58.1	115	22 AAB69601	Huntingtin minimal
38	377.5	58.1	239	22 AAB69603	Huntingtin intrabo
39	377	58.0	128	22 AAE07014	Human heavy chain
40	377	58.0	245	20 AAY06717	Antibody 12B5 sing
41	377	58.0	249	23 ABP45094	Human BlyS binding
42	376.5	57.9	127	22 AAG93584	Human anti-Rh(D) c
43	376	57.8	122	20 AAW78432	Antibody heavy cha
44	376	57.8	122	23 ABG97975	Heavy chain variab
45	376	57.8	132	23 ABG69151	Human monoclonal a

ALIGNMENTS

RESULT 1  
AAW60170  
ID AAW60170 standard; Protein; 146 AA.  
XX  
AC AAW60170;  
XX  
DT 23-SEP-1998 (first entry)  
XX  
DE Chicken Mab heavy chain variable domain sequence.  
XX  
KW Chicken: monoclonal antibody; MAB; immortalisation; immunisation;  
KW Cystic fibrosis transmembrane conductance regulator; cystic fibrosis;  
KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;  
KW transforming growth factor beta; CFTR; TGF beta.  
XX  
OS Gallus sp.  
XX  
PN WO9822510-A2.  
XX  
PD 28-MAY-1998.  
XX  
PF 18-NOV-1997; 97WO-US21077.  
XX  
PR 18-NOV-1996; 96US-0751359.  
XX  
PA (ARCH-) ARCH DEV CORP.  
PA (UABR-) UAB RES FOUND.  
XX  
PI Accavitti MAV, Michael NM, Thompson CB;  
XX WPI; 1998-312421/27.  
DR  
XX

PT Production of new monoclonal antibodies - by immunising chickens and  
 PT immortalising B cells, used for, e.g. diagnosis and passive  
 PT treatment of disease  
 XX  
 XX

XX Example 2; Page 61; 97pp; English.

CC This represents the amino acid sequence of the heavy chain variable  
 CC domain of a chicken monoclonal antibody (MAB). The invention provides a  
 CC method of producing chicken MAB against a variety of antigens. The  
 CC method comprises immunising a chicken with an antigen and isolating a  
 CC immortalising B cells. From a selected antibody-producing B cell,  
 CC nucleic acid containing antigen-binding exons of the light and heavy  
 CC chain genes is prepared. The heavy and light chain nucleic acid are  
 CC cloned separately in vectors that encode the constant and leader  
 CC regions of the heavy and light chains. The vectors are transferred to  
 CC host cells which are cultured and the MAB is isolated. Such antibodies  
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator)  
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-  
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and  
 CC carbohydrates. The MAB can be raised against antigenic determinants that  
 CC do not normally induce a response in mammals. The structure of the  
 CC chicken immunoglobulin (Ig) gene is such that even after diversification  
 CC by repeated gene conversions and maturation, the genomic DNA of the  
 CC expressed locus will always have the same L-V (leader-variable) intron  
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the  
 CC antigen-binding domain of rearranged chicken genes are known with  
 CC certainty, allowing specific amplification with a single set of primers.  
 CC The method is particularly used to produce MAB against mammalian antigens  
 CC with highly conserved epitopes. The MABs are used for separation,  
 CC detection, quantification or removal of antigens, particularly for  
 CC diagnosis, including in vivo imaging. They are useful as  
 CC immunohistochemical reagents, and for passive treatment of diseases,  
 CC such as cystic fibrosis.

XX Sequence 146 AA;

Query Match 78.1%; Score 507.5; DB 19; Length 146;  
 Best Local Similarity 80.3%; Pred. No. 8e-38;  
 Matches 102; Conservative 7; Mismatches 15; Indels 3; Gaps 1;

QY 1 AVTLDSEGGGLQTPGGALSIVCKASGDFSSYMIWVROAPGKLEYVAGIRSDGSSIIY 60  
 DB 20 AVTLDSEGGGLQTPGGALSIVCKASGDFSSYMIWVROAPGKLEYVAGIRSDGSSIIY 60  
 QY 61 GAAVKGRATISRDNQSTLRQLNNLRADTGTYYCAKSSYSGWRGSGTG----DIDAWG 79  
 DB 80 GSAVKGRATISRDNQSTLRQLNNLRADTGTYYCAKSSYSGWRGSGTG----DIDAWG 117  
 QY 118 TEIVVSS 124  
 DB 140 TEIVVSS 146

RESULT 2

AAW60171  
 ID AAW60171 standard; Protein; 145 AA.

AC AAW60171;

XX 23-SEP-1998 (first entry)

DE Heavy chain variable domain sequence of anti-CFTR 4-9.

XX Chicken; monoclonal antibody; MAB; immortalisation; immunisation;  
 KW cystic fibrosis transmembrane conductance regulator; immunisation;  
 KW B cell; passive treatment; cystic fibrosis; regulator; cystic fibrosis;  
 KW transforming growth factor beta; CFTR; TGF beta.  
 XX Gallus sp.

OS

XX WC09822510-A2.

PN

XX 28-MAY-1998.

PD

XX

PF 18-NOV-1997; 97WO-US21077.

XX 18-NOV-1996; 96US-0751359.

XX (ARCH-) ARCH DEV CORP.

PA (UABR-) UAB RES FOUND.

XX Accavitti MAV, Michael NM, Thompson CB;

XX WPI; 1998-312421/27.

XX Production of new monoclonal antibodies - by immunising chickens and

PT immortalising B cells, used for, e.g. diagnosis and passive

PT treatment of disease

XX Example 2; Page 61; 97pp; English.

XX This represents the amino acid sequence of the heavy chain variable

CC domain of anti-CFTR 4-9. The invention provides a method for producing

CC chicken monoclonal antibodies (MAB) against a variety of antigens. The

CC method comprises immunising a chicken with an antigen and isolating and

CC immortalising B cells. From a selected antibody-producing B cell,

CC nucleic acid containing antigen-binding exons of the light and heavy

CC chain genes is prepared. The heavy and light chain nucleic acid are

CC cloned separately in vectors that encode the constant and leader

CC regions of the heavy and light chains. The vectors are transferred to

CC host cells which are cultured and the MAB is isolated. Such antibodies

CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),

CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and

CC carbohydrates. The MAB can be raised against antigenic determinants that

CC do not normally induce a response in mammals. The structure of the

CC chicken immunoglobulin (Ig) gene is such that even after diversification

CC by repeated gene conversions and maturation, the genomic DNA of the

CC expressed locus will always have the same L-V (leader-variable) intron

CC and J (junction)-3' flanking sequences. Thus the sequences flanking the

CC antigen-binding domain of rearranged chicken genes are known with

CC certainty, allowing specific amplification with a single set of primers.

CC The method is particularly used to produce MAB against mammalian antigens

CC with highly conserved epitopes. The MABs are used for separation,

CC detection, quantification or removal of antigens, particularly for

CC diagnosis, including in vivo imaging. They are useful as

CC immunohistochemical reagents, and for passive treatment of diseases,

CC such as cystic fibrosis.

XX Sequence 145 AA;

Query Match 76.8%; Score 499; DB 19; Length 145;

Best Local Similarity 82.9%; Pred. No. 4.6e-37;

Matches 107; Conservative 3; Mismatches 11; Indels 8; Gaps 4;

QY 1 AVTLDSEGGGLQTPGGALSIVCKASGDFSSYMIWVROAPGKLEYVAGIRSDGSSIIY 60

DB 20 AVTLDSEGGGLQTPGGALSIVCKASGDFSSYMIWVROAPGKLEYVAGIRSDGSSIIY 60

QY 61 GAAVKGRATISRDNQSTLRQLNNLRADTGTYYCAKSSYSGWRGSGTG----DIDAWG 78

DB 79 GAAVKGRATISRDNQSTLRQLNNLRADTGTYYCAKSSYSGWRGSGTG----DIDAWG 115

QY 116 HCTEIVVSS 124

DB 137 HCTEIVVSS 145

RESULT 3

AAG78977

ID AAG78977 standard; Protein; 129 AA.

XX AAG78977;

XX 16-JAN-2002 (first entry)

DE Chicken protein #1.  
 XX Chicken; monoclonal antibody; scFv; single chain fragment of V region;  
 KW prion disease; C lambda chain.  
 KW Gallus domesticus.  
 OS JP2001238676-A.  
 XX 04-SEP-2001.  
 PD 29-FEB-2000; 2000JP-0054875.  
 XX 29-FEB-2000; 2000JP-0054875.  
 PR (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX WPI; 2001-610054/70.  
 DR  
 XX Preparing a chicken monoclonal antibody for diagnosing and treating  
 PT various diseases such as prion disease, comprises using an expression  
 PT vector  
 XX Disclosure; Fig 10; 25pp; Japanese.  
 XX The present invention relates to a method for preparing a chicken  
 CC monoclonal antibody by gene recombination. The method involves using an  
 CC expression vector prepared by introducing a gene encoding scFv (single  
 CC chain fragment of V region) of a chicken monoclonal antibody to an  
 CC expression vector in which a gene encoding chicken C lambda chain (L  
 CC chain constant region) is introduced. The chicken monoclonal antibody  
 CC can be used for diagnosing and treating various diseases such as prion  
 CC disease. The present sequence was used to illustrate the present  
 CC invention.  
 XX  
 XX Sequence 129 AA;  
 SQ  
 Query Match 75.6%; Score 491.5; DB 22; Length 129;  
 Best Local Similarity 76.7%; Pred. No. 1.9e-36;  
 Matches 99; Conservative 8; Mismatches 17; Indels 5; Gaps 1;  
 QY 1 AVTLDESGGLQTPGGALSLVCKASGDFSSYDMWVRQAPGKGLYVAGIRSDGSSYY 60  
 DB 1 AVTLDESGGLQTPGGALSLVCKASGDFSSYDMWVRQAPGKGLYVAGIRSDGSSYY 60  
 QY 61 GAAVKGRTATISRDNGQSTLRQLNLRRAEDTGYTYCAKSS----YGSWRGSGTGIDAWG 115  
 DB 61 GSAVKGRTATISRDNGQSTVRQLNLRRAEDTGYTYCAKAGCXXXXXXXXTAGSIDAWG 120  
 QY 116 HGTETIVSS 124  
 DB 121 HGTETIVSS 129  
 RESULT 4  
 AAW60173  
 ID AAW60173 standard; Protein; 147 AA.  
 XX AAW60173;  
 XX 23-SEP-1998 (first entry)  
 DT Heavy chain variable domain sequence of antibody 8 of unknown specificity.  
 DE Chicken; monoclonal antibody; MAb; immortalisation; immunisation;  
 KW cystic fibrosis transmembrane conductance regulator; cystic fibrosis;  
 KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;  
 KW transforming growth factor beta; CFTR; TGF beta.  
 XX Gallus sp.  
 OS WO9822510-A2.  
 PN  
 XX

PD 28-MAY-1998.  
 XX 18-NOV-1997; 97WO-US21077.  
 XX 18-NOV-1996; 96US-0751359.  
 PR (ARCH-) ARCH DEV CORP.  
 XX (UABR-) UAB RES FOUND.  
 PA Accavitti MAV, Michael NM, Thompson CB;  
 XX WPI; 1998-312421/27.  
 DR Production of new monoclonal antibodies - by immunising chickens and  
 XX immortalising B cells, used for, e.g. diagnosis and passive  
 PT treatment of disease  
 PT  
 XX Example 2; Page 61; 97pp; English.  
 PS  
 XX This represents the heavy chain variable domain of an antibody of unknown  
 CC specificity used as a control. The invention provides a method for  
 CC producing chicken monoclonal antibodies (MAB) against a variety of  
 CC antigens. The method comprises immunising a chicken with an antigen and  
 CC isolating and immortalising B cells. From a selected antibody-producing  
 CC B cell, nucleic acid containing antigen-binding exons of the light and  
 CC heavy chain genes is prepared. The heavy and light chain nucleic acid are  
 CC cloned separately in vectors that encode the constant and leader  
 CC regions of the heavy and light chains. The vectors are transferred to  
 CC host cells which are cultured and the MAB is isolated. Such antibodies  
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),  
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-  
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and  
 CC carbohydrates. The MAB can be raised against antigenic determinants that  
 CC do not normally induce a response in mammals. The structure of the  
 CC chicken immunoglobulin (Ig) gene is such that even after diversification  
 CC by repeated gene conversions and maturation, the genomic DNA of the  
 CC expressed locus will always have the same L-V (leader-variable) intron  
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the  
 CC antigen-binding domain of rearranged chicken genes are known with  
 CC certainty, allowing specific amplification with a single set of primers.  
 CC The method is particularly used to produce MAB against mammalian antigens  
 CC with highly conserved epitopes. The MABs are used for separation,  
 CC detection, quantification or removal of antigens, particularly for  
 CC diagnosis, including in vivo imaging. They are useful as  
 CC immunohistochemical reagents, and for passive treatment of diseases,  
 CC such as cystic fibrosis.  
 XX  
 XX Sequence 147 AA;  
 SQ  
 Query Match 75.5%; Score 491; DB 19; Length 147;  
 Best Local Similarity 78.1%; Pred. No. 2.4e-36;  
 Matches 100; Conservative 5; Mismatches 19; Indels 4; Gaps 1;  
 QY 1 AVTLDESGGLQTPGGALSLVCKASGDFSSYDMWVRQAPGKGLYVAGIRSDGSSYY 60  
 DB 20 AVTLDESGGLQTPGGALSLVCKASGDFSSYDMWVRQAPGKGLYVAGIRSDGSSYY 79  
 QY 61 GAAVKGRTATISRDNGQSTLRQLNLRRAEDTGYTYCAKSSYGSWRGS---TGIDAWGH 116  
 DB 80 APAVKGRTATISRDNGQSTLRQLNLRRAEDTGYTYCAKAGSGCSDATAGSIDAWGH 139  
 QY 117 GTEIVSS 124  
 DB 140 GTEIVSS 147  
 RESULT 5  
 AAW60172  
 ID AAW60172 standard; Protein; 141 AA.  
 XX AAW60172;  
 AC  
 XX 23-SEP-1998 (first entry)  
 DT

XX DE Heavy chain variable domain sequence of anti-CFTR 15-16.  
 XX KW Chicken; monoclonal antibody; MAB; immortalisation; immunisation;  
 KW cystic fibrosis transmembrane conductance regulator; cystic fibrosis;  
 KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;  
 KW transforming growth factor beta; CFTR; TGF beta.  
 OS Gallus sp.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 129 /note="unknown"  
 FT FT  
 PN WO9822510-A2.  
 XX PD 28-MAY-1998.  
 XX PF 18-NOV-1997; 97WO-US21077.  
 XX PR 18-NOV-1996; 96US-0751359.  
 XX PA (ARCH-) ARCH DEV CORP.  
 XX PA (UABR-) UAB RES FOUND.  
 XX PI Accavitti MAV, Michael NM, Thompson CB;  
 XX DR WPI; 1998-312421/27.  
 XX PT Production of new monoclonal antibodies - by immunising chickens and  
 PT immortalising B cells, used for, e.g. diagnosis and passive  
 PT treatment of disease  
 XX PS Example 2; Page 61; 97pp; English.  
 XX CC This represents the amino acid sequence of the heavy chain variable  
 CC domain of anti-CFTR 15-16. The invention provides a method for producing  
 CC chicken monoclonal antibodies (MAB) against a variety of antigens. The  
 CC method comprises immunising a chicken with an antigen and isolating and  
 CC immortalising B cells. From a selected antibody-producing B cell,  
 CC nucleic acid containing antigen-binding exons of the light and heavy  
 CC chain genes is prepared. The heavy and light chain nucleic acid are  
 CC cloned separately in vectors that encode the constant and leader  
 CC regions of the heavy and light chains. The vectors are transferred to  
 CC host cells which are cultured and the MAB is isolated. Such antibodies  
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),  
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-  
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and  
 CC carbohydrates. The MAB can be raised against antigenic determinants that  
 CC do not normally induce a response in mammals. The structure of the  
 CC chicken immunoglobulin (Ig) gene is such that even after diversification  
 CC by repeated gene conversions and maturation, the genomic DNA of the  
 CC expressed locus will always have the same L-V (leader-variable) intron  
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the  
 CC antigen-binding domain of rearranged chicken genes are known with  
 CC certainty, allowing specific amplification with a single set of primers.  
 CC The method is particularly used to produce MAB against mammalian antigens  
 CC with highly conserved epitopes. The MABs are used for separation,  
 CC detection, quantification or removal of antigens, particularly for  
 CC diagnosis, including in vivo imaging. They are useful as  
 CC immunohistochemical reagents, and for passive treatment of diseases,  
 CC such as cystic fibrosis.  
 XX SQ Sequence 141 AA;

Query Match 72.5%; Score 471; DB 19; Length 141;  
 Best Local Similarity 79.2%; Pred. No. 1.4e-34;  
 Matches 99; Conservative 2; Mismatches 20; Indels 4; Gaps 2;

QY 1 AVTLDESGGGLQTPGGGLSLVCKASGDFSSYDMIVRQAPGKLEYVAGIRSDGSIY 60  
 DB 20 AVTLDESGGGLQTPGGGLSLVCKASGDFSSYDMIVRQAPGKLEYVAGIRSDGSIY 60

QY 61 GAAYKGRATISRDNQSTLRQLNLNRAEDTGYCAKSSYSGWSTGDDID-ANGHGTE 119  
 DB 80 GSAVKGRATISRDNQSTLRQLNLNRAEDTGYCAKSSYSGWSTGDDID-ANGHGTE 136  
 QY 120 VIVSS 124  
 DB 137 VIVSS 141

## RESULT 6

AAY71010  
 ID AAY71010 standard; Protein; 269 AA.  
 XX AC AAY71010;

XX 29-AUG-2000 (first entry)  
 XX DE Chicken phospholamban (PLB) antibody, contractilin.

XX KW Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;  
 KW cardiomyocyte; transport peptide; penetratin; cargo peptide; chicken;  
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;  
 KW cardiant; treatment; heart failure; myocardial dysfunction.

XX OS Gallus domesticus.

XX PN WO200025804-A2.

XX PD 11-MAY-2000.

XX PF 02-NOV-1999; 99WO-US25692.

XX PR 02-NOV-1998; 98US-0106718.

XX PR 27-JUL-1999; 99US-0145883.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;  
 XX PI Scott C, Wang Y, Silverman GJ;  
 XX DR WPI; 2000-365393/31.

XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction  
 PT comprises enhancing cardiac contractility by inhibiting interaction  
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine  
 triphosphatase

XX PS Disclosure; Page 50-51; 56pp; English.

XX CC The patent discloses a method for the treatment of heart failure, using  
 CC small peptide complexes and recombinant proteins, that induces  
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB  
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.  
 CC The peptide complex comprises of transport peptide like penetratin and  
 CC cargo peptide selected from mutant PLB, native PLB or antibody against  
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a  
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac  
 CC contractility and reduces blood pressure. This method is useful for the  
 CC treatment of cardiac disease e.g. heart failure and myocardial  
 CC dysfunction. The present sequence is that of contractilin protein, a  
 CC chicken antibody peptide with hyperactive regions. This is used to raise  
 CC polyclonal PLB antibody, by immunising a chicken repeatedly with the  
 CC human PLB peptide from the cytoplasmic domain (residues 3-19).

XX SQ Sequence 269 AA;

Query Match 72.2%; Score 469.5; DB 21; Length 269;  
 Best Local Similarity 75.2%; Pred. No. 4e-34;  
 Matches 94; Conservative 9; Mismatches 19; Indels 3; Gaps 2;

QY 2 VTLDSEGGGLQTPGGGLSLVCKASGDFSSYDMIVRQAPGKLEYVAGIRSDGSIY 61  
 DB 129 VTLDSEGGGLQTPGGGLSLVCKASGDFSSYDMIVRQAPGKLEYVAGIRSDGSIY 188



CC disease. They are also useful for treating allergy, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and ige-  
 CC mediated allergic reaction, shock, stenosis, allograft rejection,  
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
 CC intervention, including angioplasty and/or stent placement in a mammal.  
 CC Humanised antibodies are also useful for inhibiting narrowing of the  
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
 CC a vessel in a mammal, and preferably associated with vascular intervention.  
 CC The present sequence is human heavy chain variable (VH) region, 038066.  
 XX  
 SQ Sequence 124 AA;

Query Match 60.3%; Score 392; DB 22; Length 124;  
 Best Local Similarity 64.2%; Pred. No. 1.4e-27;  
 Matches 79; Conservative 9; Mismatches 35; Indels 0; Gaps 0;  
 QY 2 VTLDSEGGGLQTPGGALSLVCKASGDFSSYDMIVRQAPGKLEVGIRSDGSSIIYIG 61  
 Db 2 VQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSGISGGSTYYA 61  
 QY 62 AAVKGRATISRDNGQSTLRQLNLRAEDTGYTCYCAKSSYSGWRGSGTGDIDAWHGTEVI 121  
 Db 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYICANDYSGRYFTVATDVGOGTTVT 121  
 QY 122 VSS 124  
 Db 122 VSS 124

RESULT 9  
 AAM24101  
 ID AAM24101 standard; Protein; 384 AA.  
 AC AAM24101;  
 DT 12-OCT-2001 (first entry)  
 DE Human EST encoded protein SEQ ID NO: 1626.  
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition.  
 OS Homo sapiens.  
 XX  
 XX WO200154477-A2.  
 XX  
 XX PD 02-AUG-2001.  
 XX  
 XX PF 25-JAN-2001; 2001WO-US02687.  
 XX  
 XX PR 25-JAN-2000; 2000US-0491404.  
 XX PR 17-JUL-2000; 2000US-0617746.  
 XX PR 03-AUG-2000; 2000US-0631454.  
 XX PR 15-SEP-2000; 2000US-0663870.  
 XX  
 XX PA (HYSE-) HYSEQ INC.  
 XX  
 XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 XX DR WPI; 2001-476164/51.  
 XX DR N-PSDB; AAH98760.  
 XX  
 XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 XX PT antibodies and research use -  
 XX  
 XX PS Claim 20; Page 1102-1103; 1275pp; English.  
 XX

The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a  
 XX protein of the invention.  
 SQ Sequence 384 AA;

Query Match 59.9%; Score 389.5; DB 22; Length 384;  
 Best Local Similarity 62.9%; Pred. No. 8.5e-27;  
 Matches 83; Conservative 9; Mismatches 31; Indels 9; Gaps 2;  
 QY 2 VTLDSEGGGLQTPGGALSLVCKASGDFSSYDMIVRQAPGKLEVGIRSDGSSIIYIG 61  
 Db 21 VQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSGISGGSTYYA 80  
 QY 62 AAVKGRATISRDNGQSTLRQLNLRAEDTGYTCYCAKSSYSGWRGSGTGDIDAWHGTEVI 112  
 Db 81 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYICANDYSGRYFTVATDVGOGTTVT 140  
 QY 113 AMHGTEVI 124  
 Db 141 VMGQGTIVSS 152

RESULT 10  
 ABG69154  
 ID ABG69154 standard; Protein; 132 AA.  
 AC ABG69154;  
 DT 07-OCT-2002 (first entry)  
 DE Human monoclonal antibody BT33/A6 VH region A6VH-L1 library.  
 KW Monoclonal antibody; BT33/A6; phage display; panning; framework region;  
 KW Heavy chain variable region; CDR; complementarity determining region;  
 KW combinatorial library; mutant; mutin.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200251870-A2.  
 XX  
 XX PD 04-JUL-2002.  
 XX  
 XX PF 21-DEC-2001; 2001WO-CA01845.  
 XX  
 XX PR 22-DEC-2000; 2000US-258031P.  
 XX  
 XX PA (GRAD/) GRAD C.  
 XX PA (ENTW/) ENTWISTLE J.  
 XX PA (TANH/) TANHA J.  
 XX PA (NARA/) NARANG S.  
 XX PA (DANM/) DAN M.  
 XX PA (MACK/) MACKENZIE C R.  
 XX  
 XX PI Entwistle J, Tanha J, Narang S, Dan M, Mackenzie CR;  
 XX  
 XX DR WPI; 2002-575370/61.  
 XX DR N-PSDB; ABK98583.  
 XX  
 XX PT New libraries comprising a repertoire of nucleic acid sequences  
 XX PT encoding a polypeptide with a VH with CDR for expressing immunoglobulin  
 XX PT heavy chain binding domains for panning against the target ligand -  
 XX  
 XX PS Disclosure; Fig 10; 98pp; English.  
 XX

The invention relates to a library comprising a repertoire of nucleic  
 CC acid sequences each encoding a polypeptide with a variable heavy (VH)  
 CC domain with a Complementarity Determining Region (CDR) differing at  
 CC least in CDR and comprising at least one of the amino acids 6-A, 23-A,



CC 82a-N, 93-A or 108-Q, in comparison to the parent human monoclonal  
 CC antibody A6 heavy chain domain. The library (e.g. a combinatorial  
 CC library for phage display) may comprise at least the framework region of  
 CC A6 VH including the CDR region containing the target amino acids above.  
 CC The libraries are useful in expressing a series of potential heavy chain  
 CC binding domains for panning against the target ligand. The amino acid  
 CC residues 6, 23, 82a, 93, and 108, particularly when combined, are  
 CC useful in augmenting the solubility properties of a parental VH ligand  
 CC binding fragment, preferably one like A6, which has useful solubility  
 CC properties in producing a library of dAb variants for panning against a  
 CC target ligand. The present sequence represents the human monoclonal  
 CC antibody BT33/A6 (or just A6) heavy chain variable domain variant  
 CC protein (either a created mutant or a representative of a combinatorial  
 CC library of mutants).

SQ Sequence 132 AA;  
 Query Match 59.7%; Score 388; DB 23; Length 132;  
 Best Local Similarity 59.5%; Pred. No. 3.4e-27;  
 Matches 78; Conservative 12; Mismatches 33; Indels 8; Gaps 1;  
 QY 2 VTLDSEGGGLQTPGGALSILVCKASGDFSSYDMIVWVROAPKGLVYAGIRSDGSSIIYG 61  
 DB 2 VQLQASGGGLVOPGGSLRLSCAASGFTFSYAMHWVROAPKGLVYSAISNGSGSTYYA 61  
 QY 62 AAVKGRATISRDNGQSTLRQLNLRRAEDTGYTCYAK-----SSYGSWRGSGTGDDA 113  
 DB 62 DSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAKDLKVEYDSSGYNNNNNNFDDI 121  
 QY 114 WGHGTEIVVSS 124  
 DB 122 WGQGTQTVVSS 132

RESULT 11  
 ABJ36939  
 ID ABJ36939 standard; Protein; 177 AA.  
 XX  
 AC ABJ36939;  
 DT 01-MAY-2003 (first entry)  
 XX  
 DE Anti-CD40 monoclonal antibody related protein SEQ ID No 64.  
 DE  
 KW Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;  
 KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;  
 KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;  
 KW immunosuppressor; anti-tumour agent; immunosuppressant; allergy;  
 KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.  
 XX  
 OS Unidentified.  
 OS  
 XX WO200288186-A1.  
 XX  
 PD 07-NOV-2002.  
 XX  
 XX 26-APR-2002; 2002WO-JP04292.  
 XX  
 XX 27-APR-2001; 2001WO-US13672.  
 PR  
 PR 11-MAY-2001; 2001JP-0142482.  
 PR  
 PR 05-OCT-2001; 2001JP-0310535.  
 PR  
 PR 26-OCT-2001; 2001US-0040244.  
 XX  
 XX (KIRI ) KIRIN BEER KK.  
 XX  
 XX MIKAYAMA T, Yoshida H, Force WR, Chen X, Takahashi N;  
 PI  
 XX WPI; 2003-120463/11.  
 DR  
 DR N-PSDB; ABT31881.  
 XX  
 XX Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,  
 PT or functional fragment, is useful in the treatment of e.g. autoimmune  
 PT diseases or cancer

XX  
 PS Claim 15; Page 59; 94pp; Japanese.  
 CC  
 CC The invention relates to an antibody to human CD40, or its functional  
 CC fragment, has at least one of the following properties: acting on  
 CC dendritic cells to produce IL-12 in the presence of LPS  
 CC (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic  
 CC cells to activate maturity of the dendritic cells with high G28-5  
 CC antibody; and activating CD95 expression with high G28-5 antibody against  
 CC B cell line. Such antibodies or functional fragments can be used as  
 CC immunosuppressants, anti-tumour agents, immunosuppressants, and as remedies  
 CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors  
 CC syndrome. This sequence represents a protein relating to the anti-CD40  
 CC monoclonal antibody of the invention.

SQ Sequence 177 AA;  
 Query Match 59.2%; Score 385; DB 24; Length 177;  
 Best Local Similarity 64.8%; Pred. No. 8.8e-27;  
 Matches 81; Conservative 8; Mismatches 32; Indels 4; Gaps 2;  
 QY 2 VTLDSEGGGLQTPGGALSILVCKASGDFSSYDMIVWVROAPKGLVYAGIRSDGSSIIYG 61  
 DB 21 VQLLESGGLVOPGGSLRLSCAASGFTFSYAMSWVROAPKGLVYSAISNGSGSTYYA 80  
 QY 62 AAVKGRATISRDNGQSTLRQLNLRRAEDTGYTCYAKSS--YGSWRGSGTGDDIDAWHGTE 119  
 DB 81 DSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAKDGYYGS--GSYGYFDYWGQGT 138  
 QY 120 VIVSS 124  
 DB 139 VIVSS 143

RESULT 12  
 ABG69150  
 ID ABG69150 standard; Protein; 132 AA.  
 XX  
 AC ABG69150;  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Human monoclonal antibody BT33/A6 VH region variant A6VH-L1.  
 DE  
 KW Monoclonal antibody; BT33/A6; phage display; panning; framework region;  
 KW Heavy chain variable region; CDR; complementarity determining region;  
 KW combinatorial library; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200251870-A2.  
 XX  
 PD 04-JUL-2002.  
 XX  
 XX 21-DEC-2001; 2001WO-CA01845.  
 PF  
 XX 22-DEC-2000; 2000US-258031P.  
 PR  
 XX (GRAD/) GRAD C.  
 PA (ENTW/) ENTWISTLE J.  
 PA (TANH/) TANHA J.  
 PA (NARA/) NARANG S.  
 PA (DANM/) DAN M.  
 PA (MACK/) MACKENZIE C R.  
 XX  
 XX Entwistle J, Tanha J, Narang S, Dan M, Mackenzie CR;  
 PI  
 XX WPI; 2002-575370/61.  
 DR  
 DR N-PSDB; ABK98579.  
 XX  
 XX New libraries comprising a repertoire of nucleic acid sequences  
 PT encoding a polypeptide with a VH with CDR for expressing immunoglobulin

PT heavy chain binding domains for panning against the target ligand -  
 XX Claim 12; Fig 2; 98pp; English.  
 XX The invention relates to a library comprising a repertoire of nucleic  
 CC acid sequences each encoding a polypeptide with a variable heavy (VH)  
 CC domain with a Complementarity Determining Region (CDR) differing at  
 CC least in CDR and comprising at least one of the amino acids 6-A, 23-A,  
 CC 82a-N, 93-A or 108-Q, in comparison to the parent human monoclonal  
 CC antibody A6 heavy chain domain. The library (e.g. a combinatorial  
 CC library for phage display) may comprise at least the framework region of  
 CC A6 VH including the CDR region containing the target amino acids above.  
 CC The libraries are useful in expressing a series of potential heavy chain  
 CC binding domains for panning against the target amino acids above.  
 CC residues 6, 23, 82a, 93, and 108, particularly when combined, are  
 CC useful in augmenting the solubility properties of a parental VH ligand  
 CC binding fragment, preferably one like A6, which has useful solubility  
 CC properties in producing a library of dAb variants for panning against a  
 CC target ligand. The present sequence represents the human monoclonal  
 CC antibody B13/A6 (or just A6) heavy chain variable domain variant  
 CC protein (either a created mutant or a representative of a combinatorial  
 CC library of mutants).  
 XX Sequence 132 AA;

Query Match 59.1%; Score 384; DB 23; Length 132;  
 Best Local Similarity 60.3%; Pred. No. 7.8e-27;  
 Matches 79; Conservative 10; Mismatches 34; Indels 8; Gaps 1;  
 QY 2 VTLDSEGGGLQTPGGLSLVCKASGDFSSYDMHWRAQPGKLEYVAGIRSDGSSIIYG 61  
 Db 2 VQLQASGGGLVQPGSLRLSCAASGFTFSYAMHWRAQPGKLEYVSAISSNGSTYYA 61  
 QY 62 AAVKGRATISRDNGQSTLRQLNNLRAEDTGTYYCAK-----SSYGSWRGSGTGDDA 113  
 Db 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKRLKVEYDSSGYVSRFGAFDI 121  
 QY 114 WGHGTEIVYSS 124  
 Db 122 WGQGTQTVTSS 132

RESULT 13  
 ABP45508  
 ID ABP45508 standard; Protein; 252 AA.  
 AC ABP45508;  
 XX 19-AUG-2002 (first entry)  
 DE Human BlyS binding scFv SEQ ID 1519.  
 XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 XX WO200202641-A1.  
 PN 10-JAN-2002.  
 PD 10-JAN-2002.  
 XX 15-JUN-2001; 2001WO-US19110.  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
 XX the diagnosis and treatment of cancers and immune disorders -  
 PS Claim 1; Page 2215-2216; 3148pp; English.  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
 CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BlyS. They may also be  
 CC administered to treat diseases associated with aberrant BlyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX Sequence 252 AA;

Query Match 58.9%; Score 383; DB 23; Length 252;  
 Best Local Similarity 63.4%; Pred. No. 2e-26;  
 Matches 78; Conservative 9; Mismatches 36; Indels 0; Gaps 0;  
 QY 2 VTLDSEGGGLQTPGGLSLVCKASGDFSSYDMHWRAQPGKLEYVAGIRSDGSSIIYG 61  
 Db 2 VQLQESGGVQPGSLRLSCAASGFTFSYGHVWRQAPGKLEWVAVLSYDGSNKYYA 61  
 QY 62 AAVKGRATISRDNGQSTLRQLNNLRAEDTGTYYCAKSSYGSWRGSGTGDDA HGHGTEVI 121  
 Db 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKROYDILTGYGDFYWGQGTMTV 121  
 QY 122 VSS 124  
 Db 122 VSS 124

RESULT 14  
 ABP44985  
 ID ABP44985 standard; Protein; 247 AA.  
 AC ABP44985;  
 XX 19-AUG-2002 (first entry)  
 DE Human BlyS binding scFv SEQ ID 996.  
 XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 XX WO200202641-A1.  
 PN 10-JAN-2002.  
 PD 10-JAN-2002.  
 XX 15-JUN-2001; 2001WO-US19110.

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XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
XX * Claim 1; Page 1590-1591; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys in
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
XX SQ Sequence 247 AA;
XX
XX Query Match 58.8%; Score 382; DB 23; Length 247;
XX Best Local Similarity 61.8%; Pred. No. 2.4e-26;
XX Matches 76; Conservative 11; Mismatches 36; Indels 0; Gaps 0
XX
XX QY 2 VTLDSEGGGLTPGGALSLVCKASGDFPSSDTMTLWVROAPKGLEYVAGIRSDGSIYVG 61
XX ||| ||||: ||: || ||| |||| |||| |||| |||| ||||: || |||
XX 2 VTLDSEGGGVVQGRSLRLSCAASGFTFSSYGMHWVROAPKGLEWVAISGSGGSTYYA 61
XX |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
XX 62 AAVKGRATISRDNGOSTLRLQLNLRAEDTCTYYCAKSSYGSWRGSTDIDAWHGTEVI 121
XX |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
XX 62 DSVKGRFTISRDNSKNTLYLQMSLRADETAVYYCAKSGYDILGILGYLGMVWGQGTWVT 121
XX |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
XX QY 122 VSS 124
XX |||
XX Db 122 VSS 124
XX
XX RESULT 15
XX AAB39519
XX ID AAB39519 standard; Protein; 115 AA.
XX
XX AC AAB39519;
XX
XX XX
XX DT 05-FEB-2001 (first entry)
XX
XX XX Anti-IL12 antibody H chain variable region amino acid sequence SEQ ID 35.
XX
XX Human; neutralising antibody; interleukin-12; IL-12; antinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritis;
XX antisclerotic; neuroprotective; antipsoriatic; antischmatic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.
XX
XX OS Homo sapiens.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:00:29 ; Search time 31.3125 Seconds  
(without alignments)  
547.464 Million cell updates/sec

Title: US-10-083-424A-26

Perfect score: 563

Sequence: 1 ALTPSSVSANPGTKVITC.....GSFSSYVILGAGTTLVL 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459.5	81.6	269	21	AAV71010
2	449.5	79.8	126	19	AAW60167
3	427	75.8	105	22	AAG78978
4	426.5	75.8	126	19	AAW60166
5	426	75.7	125	19	AAW60168
6	423.5	75.2	124	19	AAW60169
7	319.5	56.7	212	24	ABR01489
8	318.5	56.6	108	23	ABBS7560
9	318.5	56.6	212	24	ABR01497
					Chicken phospholamban
					Light chain variab
					Chicken protein #2
					Chicken Mab light
					Light chain variab
					Light chain variab
					Human anti-TIMP-1
					HLA-DR-specific pr
					Human anti-TIMP-1

10	318	56.5	111	18	AAW13528	Anti-melanoma ligh
11	318	56.5	249	23	ABP45301	Human BlyS binding
12	316.5	56.2	108	23	AAO18431	Anti-GD2 antibody
13	315.5	56.0	245	22	ABAB67622	Human leukocyte an
14	315	56.0	251	23	ABP45545	Human BlyS binding
15	315	56.0	251	23	ABP45829	Human BlyS binding
16	314.5	55.9	245	24	ABR67619	Human leukocyte an
17	312	55.4	215	22	ABR01491	Human anti-TIMP-1
18	312	55.4	255	23	ABP45145	Human BlyS binding
19	311.5	55.3	245	22	ABAB67620	Human leukocyte an
20	311	55.2	211	24	ABR01471	Human anti-TIMP-1
21	311	55.2	211	24	ABR01495	Human anti-TIMP-1
22	310.5	55.2	245	22	ABAB67617	Human leukocyte an
23	310	55.1	258	23	ABP45249	Human BlyS binding
24	309.5	55.0	245	22	ABAB67618	Human leukocyte an
25	309	54.9	108	17	AAH88719	Human antibody lam
26	309	54.9	123	24	AAO19680	P aeruginosa MEP a
27	309	54.9	211	24	ABR01472	Human anti-TIMP-1
28	308.5	54.8	245	22	ABAB67621	Human leukocyte an
29	308	54.7	109	23	AAU83808	MS-GPC-10 light ch
30	308	54.7	109	23	ABBS7568	HLA-DR-specific pr
31	308	54.7	111	23	AAO18430	Anti-GD2 antibody
32	308	54.7	245	24	ABP60521	APRIL binding scFv
33	308	54.7	248	23	ABP44850	Human BlyS binding
34	308	54.7	258	23	ABP45018	Human BlyS binding
35	307.5	54.6	110	23	AAO18434	Anti-GD2 antibody
36	307.5	54.6	245	22	ABAB67623	Human leukocyte an
37	307	54.5	111	21	AAH82529	Carcinoembryonic a
38	307	54.5	215	24	ABR01480	Human anti-TIMP-1
39	306.5	54.4	214	24	ABR01470	Human anti-TIMP-1
40	306.5	54.4	245	23	ABP45853	Human BlyS binding
41	306.5	54.4	252	23	ABP45538	Human BlyS binding
42	306.5	54.4	252	23	ABP45981	Human BlyS binding
43	306	54.4	215	24	ABR01500	Human anti-TIMP-1
44	306	54.4	246	23	ABP46066	Human BlyS binding
45	306	54.4	253	23	ABP45848	Human BlyS binding

ALIGNMENTS

RESULT 1  
AAV71010  
ID AAV71010 standard; Protein; 269 AA.  
AC AAV71010;  
XX  
XX 29-AUG-2000 (first entry)  
DT  
XX Chicken phospholamban (PLB) antibody, contractilin.  
DE Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;  
KW cardiomyocyte; transport peptide; penetratin; cargo peptide; chicken;  
KW contractilin; cardiac contractility; inhibitor; cardiac disease;  
KW cardiant; treatment; heart failure; myocardial dysfunction.  
XX  
OS Gallus domesticus.  
XX  
XX WO200025804-A2.  
PN  
XX  
PD 11-MAY-2000.  
XX  
XX 02-NOV-1999; 99WO-US25692.  
XX  
PR 02-NOV-1998; 98US-0106718.  
PR 27-JUL-1999; 99US-0145883.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;  
PI Scott C, Wang Y, Silverman GJ;  
XX  
DR WPI; 2000-365393/31.

Production of new monoclonal antibodies - by immunising chickens and immortalising B cells, used for, e.g. diagnosis and passive treatment of disease

X







KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.  
 XX Homo sapiens.  
 XX WO2000286085-A2.  
 XX 31-OCT-2002.  
 XX 24-APR-2002; 2002WO-US12801.  
 XX 24-APR-2001; 2001US-285683P.  
 XX (FARB ) BAYER CORP.  
 XX (MORP-) MORPHOSYS AG.  
 XX Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;  
 XX WPI; 2003-129114/12.  
 DR N-PSDB; ABZ74846.  
 XX New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1)  
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder  
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate  
 PT hypertrophy or lung cancer -  
 XX Claim 21; Page 138; 228pp; English.  
 XX The invention relates to a novel purified preparation of a human  
 CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)  
 CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of  
 CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and  
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant  
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
 CC activity of a TIMP-1. It is especially useful for ameliorating the  
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic  
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon  
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
 CC elevated. The sequences shown in ABR01460-ABR01501 represent the light  
 CC chain regions of a human anti-TIMP-1 antibody of the invention.  
 XX Sequence 212 AA;  
 SQ  
 Query Match 56.7%; Score 319.5; DB 24; Length 212;  
 Best Local Similarity 60.7%; Pred. No. 7.1e-19;  
 Matches 65; Conservative 10; Mismatches 29; Indels 3; Gaps 2;  
 Qy 2 LTQPSVSANPGETVKITCSGGSYAGSYGYGWYQKAPASAPVTVIYDNTNRPSNIPSR 61  
 DB 4 LTQPPSVSVPAGQTARISCSGDA--LGDKYASWYQK-PGQAPVLVIYDSDRPSGIPER 60  
 Qy 62 FSGSLSGSTNTITIGQVQDEADYVYCGSPDSYVGLGATTTVL 108  
 DB 61 FSGNSGNTATLTISGTAQDEADYVYCSYDLRYSHVFGGKTLTVL 107  
 RESULT 8  
 ABB57560  
 ID ABB57560 standard; Peptide; 108 AA.  
 XX ABB57560;  
 AC ABB57560;  
 XX 18-MAR-2002 (first entry)  
 DT  
 XX HLA-DR-specific protein MS-GPC5 VL sequence.  
 DE  
 XX Immunomodulatory human MHC class II antigen-binding protein; HLA;  
 KW human leukocyte antigen; immune system; immunosuppression; antibody;  
 KW major histocompatibility complex; antirheumatic; antiarthritic;

KW neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;  
 KW immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;  
 KW thyromimetic; hepatotropic; immune response suppressor; narcolepsy;  
 KW rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;  
 KW Grave's disease; insulin-dependent diabetes; Hashimoto's disease;  
 KW systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;  
 KW transplant rejection; graft versus host disease; pemphigus vulgaris;  
 KW glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;  
 KW irritable bowel disease; Sjogren's syndrome.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200187338-A1.  
 XX 22-NOV-2001.  
 XX 14-MAY-2001; 2001WO-US15626.  
 XX 12-MAY-2000; 2000EP-0110063.  
 XX 06-OCT-2000; 2000US-238762P.  
 XX (GPCB-) GPC BIOTECH AG.  
 XX (MORP-) MORPHOSYS AG.  
 XX Nagy Z, Tesar M, Thomassen-Wolf E;  
 XX WPI; 2002-075289/10.  
 XX Composition for suppressing immune response, treating diseases of  
 PT immune system, has polypeptide comprising antibody-based  
 PT antigen-binding domain of human composition, which binds antigen  
 PT expressed on a cell surface -  
 XX Example; Fig 15; 139pp; English.  
 XX The present invention describes a composition (I), comprising a  
 CC polypeptide comprising an antibody-based antigen-binding domain of human  
 CC composition with binding specificity for an antigen expressed on the  
 CC surface of a cell, where treating cells expressing the antigen with the  
 CC polypeptides leads to suppression of an immune response, and the IC50 for  
 CC the suppression of immune response is 1 microm or less. (I) has  
 CC antineumatic, antiarthritic, neuroprotective, antiinflammatory,  
 CC antidiabetic, antipsoriatic, immunosuppressive, dermatological,  
 CC antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and  
 CC can be used as a suppressor of immune response. (I) is useful for  
 CC suppressing activation or proliferation of a cell of the immune system,  
 CC suppressing IL-2 secretion by a cell, the interaction of a cell of the  
 CC immune system with another cell, immunosuppressing a patient and for  
 CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR  
 CC on the surface of the cell, where neither cytotoxic entities nor  
 CC immunological mechanisms are needed to cause or lead to the killing.  
 CC (I) optionally linked to cytotoxic or immunogenic agent) is useful for  
 CC preparing a pharmaceutical preparation for the treatment of rheumatoid  
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,  
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus  
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus  
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,  
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary  
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.  
 CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in  
 CC the exemplification of the present invention.  
 XX Sequence 108 AA;  
 SQ  
 Query Match 56.6%; Score 318.5; DB 23; Length 108;  
 Best Local Similarity 59.8%; Pred. No. 4.3e-19;  
 Matches 64; Conservative 12; Mismatches 28; Indels 3; Gaps 2;  
 Qy 2 LTQPSVSANPGETVKITCSGGSYAGSYGYGWYQKAPASAPVTVIYDNTNRPSNIPSR 61  
 DB 4 LTQPPSVSVPAGQTARISCSGDA--LGDKYASWYQK-PGQAPVLVIYDSDRPSGIPER 60

QY 62 FSGSLGSGNTLITGVQVEDEAVYCGSFSSVYVILGAGTTLTVL 108  
 DB 61 FSGNSGNTATLTISGTADEADYVQSYDNDVDSVFGGKTLTVL 107

RESULT 9  
 ID ABR01497 standard; Protein; 212 AA.  
 AC ABR01497;  
 DT 16-APR-2003 (first entry)  
 DE Human anti-TIMP-1 antibody light chain #38.  
 XX Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;  
 KW matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatotropic;  
 KW alcoholic liver disease; cytostatic; nephrotropic; cardiant; liver fibrosis;  
 KW lupus nephritis; glomerulosclerotic renal disease; acute coronary syndrome;  
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.  
 OS Homo sapiens.

XX WO200286085-A2.  
 XX 31-OCT-2002.  
 XX 24-APR-2002; 2002WO-US12801.  
 XX 24-APR-2001; 2001US-285683P.  
 PA (FARB ) BAYER CORP.  
 PA (MORP-) MORPHOSYS AG.  
 XX Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;  
 WPI; 2003-129114/12.  
 DR N-PSDB; ABZ74854.

XX New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)  
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder  
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate  
 PT hypertrophy or lung cancer

XX Claim 21; Page 143-144; 228pp; English.

XX The invention relates to a novel purified preparation of a human  
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)  
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of  
 CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and  
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant  
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic  
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon  
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
 CC elevated. The sequences shown in ABR01460-ABR01501 represent the light  
 CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 212 AA;

Query Match 56.6%; Score 318.5; DB 24; Length 212;  
 Best Local Similarity 60.7%; Pred. No. 8.6e-19;  
 Matches 65; Conservative 11; Mismatches 28; Indels 3; Gaps 2;

QY 2 LTPQSSVSNAPGETVKITCSGGSYAGSYGYWQKAPASAPVTVVDNTNRPNSIPSR 61  
 DB 4 LIQPFVSVPQGTARISCSGDA--LGDKYASWYQOK-PGQAPVLVIYDDSDRPSGIPR 60

QY 62 FSGSLGSGNTLITGVQVEDEAVYCGSFSSVYVILGAGTTLTVL 108  
 DB 61 FSGNSGNTATLTISGTADEADYVQSYDNDVDSVFGGKTLTVL 107

RESULT 10  
 ID AAW13528 standard; protein; 111 AA.  
 AC AAW13528;  
 DT 28-OCT-1997 (first entry)  
 DE Anti-melanoma light chain antibody clone V373.  
 XX Human; monoclonal antitumour antibody; peripheral blood lymphocyte;  
 KW cancer; tumourigenesis; anticancer vaccine.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Region 23..35  
 FT /label= CDR1  
 FT Region 51..57  
 FT /label= CDR2  
 FT Region 90..100  
 FT /label= CDR3

XX WO9702479-A2.  
 XX 23-JAN-1997.  
 XX 28-JUN-1996; 96WO-IB01032.  
 XX 30-JUN-1995; 95US-0497647.  
 XX (UYUA ) UNIV YALE.  
 XX Cai X, Garen A;  
 XX WPI; 1997-109061/10.

XX Prodn. of human monoclonal anti-tumour antibodies - by screening a  
 PT fusion phase library produced using peripheral blood lymphocytes  
 PT from a cancer patient

XX Claim 19; Page 65; 82pp; English.

XX A process for isolating and synthesising human monoclonal anti-tumour  
 CC antibodies has been produced. The process involves: (a) constructing at  
 CC least one fusion phase library from the peripheral blood lymphocytes  
 CC (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in  
 CC the phase library in a binding assay with cultured tumour cells of the  
 CC same type as the patient's tumour; (c) removing extraneous antibodies by  
 CC absorption against normal human cells; (d) cloning the phase selected in  
 CC step (b) and (c); (e) assaying the specificity of the cloned phase by  
 CC incubating the phase with at least two types of cultured normal cells;  
 CC and (f) further testing the specificity of cloned phase that do not bind  
 CC to either cell line of cultured normal cells in further binding assays  
 CC to cultured tumour cells derived from more than one other tumour that is  
 CC not the patient's tumour. The present sequence represents a human light  
 CC chain antibody, from an scv antibody fusion phase library, produced by  
 CC a method as described above. The antibodies produced can be used for  
 CC diagnostic and therapeutic applications and for isolating tumour  
 CC antigens for studying tumourigenesis or for use as anti-cancer vaccines.  
 CC The human antibodies have low immunogenicity in humans compared to  
 CC murine monoclonal antibodies (MABs). Since the antibodies are isolated  
 CC from fusion phase libraries, their affinity and specificity for a  
 CC tumour cell line can be improved by genetic manipulations.

XX Sequence 111 AA;

```

XX SQ Sequence 249 AA;
Query Match 56.5%; Score 318; DB 23; Length 249;
Best Local Similarity 64.2%; Pred. No. 1.le-18;
Matches 70; Conservative 6; Mismatches 27; Indels 6; Gaps 4;

QY 2 LTQPPSVSANPGETVKITCGGSGYAGSYYYGWYQKAPASAPVTVIYDNTNRPSNIPSR 61
Db 144 LTQPPSVSAAPQTVRITCGDGS--LRSYVASWYQK-PGQAPVLVIYKNNRPSGIPDR 200
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFDDSS--YVGILGAGTTLTVL 108
Db 201 FSGSSSGNTASLTITGAQADEADYYCNSRDSGNHV-VFGGGTKLTVL 248

RESULT 12
AAOI8431
ID AAOI8431 standard; protein; 108 AA.
XX
XX AAOI8431;
AC
XX
DT 11-OCT-2002 (first entry)
XX
XX Anti-GD2 antibody light chain #8.
DE
DE Anti-GD2 antibody; neuroectodermal tumour; cancer; neuroblastoma;
KW melanoma; vaccine; gene therapy; cytostatic; disialoganglioside GD2.
KW
XX Homo sapiens.
OS Synthetic.
OS
XX DEI0059930-A1.
XX
XX 29-MAY-2002.
PD
XX
XX 23-NOV-2000; 2000DE-1059930.
XX
XX 23-NOV-2000; 2000DE-1059930.
XX
XX (FISC/) FISCHER P.
PA (UTTE/) UTTENREUTHER-FISCHER M.
XX
XX Uttenreuther-Fischer M, Krueger J;
PI
XX
XX WPI; 2002-510006/55.
XX
XX Composition for treating tumors that produce disialoganglioside GD2,
PT comprises human antibody fragment able to induce anti-idiotypic
PT antibodies
XX
XX Claim 3; Fig 7A; 14pp; German.
XX
XX The present invention relates to a composition for treating tumours
CC positive for disialoganglioside GD2 which is based on human antibody
CC fragments that activate the immune system against GD2, specifically by
CC inducing anti-GD2 antibodies. The composition can be used in the
CC treatment of neuroblastoma and melanoma. The present sequence is an
CC anti-GD2 antibody light chain.
XX
XX SQ Sequence 108 AA;
Query Match 56.2%; Score 316.5; DB 23; Length 108;
Best Local Similarity 59.8%; Pred. No. 6.3e-19;
Matches 64; Conservative 11; Mismatches 31; Indels 1; Gaps 1;

QY 2 LTQPPSVSANPGETVKITCGGSGYAGSYYYGWYQKAPASAPVTVIYDNTNRPSNIPSR 61
Db 2 LTQPPSVSAAPQKQVTISCGSSNTGNVSVYQQ-LPGTAPKLLIYDNRKPSGIPDR 60
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFDDSSYVVGILGAGTTLTVL 108
Db 61 FSGSKSGP SATIGITGLGTGDEADYCGTWDSSLVSWVFGGTKLTVL 107

```

RESULT 13  
AAB67622  
ID AAB67622 standard; Protein; 245 AA.  
AC AAB67622;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_6.  
XX  
KW Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;  
KW miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200114558-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 28-AUG-2000; 2000WO-EP08388.  
XX  
PR 26-AUG-1999; 99EP-0116691.  
XX  
PA (MORP-) MORPHOSYS AG.  
XX  
PI Kretschmar T, Tesar M, Marget M, Kroenke M;  
XX WPI; 2001-218451/22.  
XX  
PT Novel isolated human immunoglobulin or functional immunoglobulin  
PT fragment specific for human leukocyte antigen Cw6, useful for treatment  
XX of humans and for human leukocyte antigen phenotyping  
XX  
PS Claim 3; Fig 1; 23pp; English.  
XX  
CC AAB67617-23 represent single chain antibody (scFv) fragments which  
CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are  
CC derived from a synthetic human combinatorial antibody library based on  
CC molecular consensus frameworks and CDRs randomised with trinucleotides.  
CC The specification describes a human immunoglobulin fragments specific  
CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in  
CC studies of natural killer cell silencing as well as miscarriages.  
CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.  
CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin  
CC fragments are useful for the preparation of a pharmaceutical for the  
CC treatment of humans. They are also useful for HLA phenotyping.  
XX  
SQ Sequence 245 AA;  
Query Match 56.0%; Score 315.5; DB 22; Length 245;  
Best Local Similarity 60.7%; Pred. No. 1.8e-18;  
Matches 65; Conservative 10; Mismatches 29; Indels 3; Gaps 2;  
QY 2 LTQPSVSNPGEVTKITCGSGGSYAGSYGYGKAPASAPVTIYDNTNPSNIPSR 61  
DB 141 LTQPSVSNPGEVTKITCGSGGSYAGSYGYGKAPASAPVTIYDNTNPSNIPSR 61  
QY 62 FSGSLSGSTNTLTITGQVDEAVYCGSFDSSYVGIAGTTLTVL 108  
DB 198 FSGNSGNTALTITGQVDEAVYCGSFDSSYVGIAGTTLTVL 244  
RESULT 14  
ABP45545  
ID ABP45545 standard; Protein; 251 AA.  
XX  
AC ABP45545;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human BlyS binding scFv SEQ ID 1556.

XX  
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
PR 16-JUN-2000; 2000US-212210P.  
PR 17-OCT-2000; 2000US-240816P.  
PR 16-MAR-2001; 2001US-276248P.  
PR 21-MAR-2001; 2001US-277379P.  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
XX the diagnosis and treatment of cancers and immune disorders  
XX  
PS Claim 1; Page 2259-2261; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
CC and so may be used to detect and quantitate the presence of BlyS in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of BlyS. They may also be  
CC administered to treat diseases associated with aberrant BlyS expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC acquired immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
SQ Sequence 251 AA;  
Query Match 56.0%; Score 315; DB 23; Length 251;  
Best Local Similarity 58.3%; Pred. No. 2e-18;  
Matches 63; Conservative 14; Mismatches 29; Indels 2; Gaps 2;  
QY 2 LTQPSVSNPGEVTKITCGSGGSYAGSYGYGKAPASAPVTIYDNTNPSNIPSR 61  
DB 144 VTQPPAVSAAPGQKVTISCGSSNIGSYVVSQYQ-LPGTAPKLIYDNRKPSGIPR 202  
QY 62 FSGSLSGSTNTLTITGQVDEAVYCGSFDSSY-VGILGAGTTLTVL 108  
DB 203 FSVSKSGTSTLALTITGQVDEAVYCGSFDSSY-VGILGAGTTLTVL 250  
RESULT 15  
ABP45829  
ID ABP45829 standard; Protein; 251 AA.  
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AC ABP45829;  
XX

[illegible]

Search completed: September 3, 2003, 12:09:20  
Job time : 31.3125 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:03:39 ; Search time 9.9375 Seconds  
(without alignments)  
459.831 Million cell updates/sec

Title: US-10-083-424A-26  
Perfect score: 563  
Sequence: 1 ALTOPSSVSANPGETVKITC.....GSPDSSVVGILGAGTTLTVL 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCITUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	449.5	79.8	126	3	US-08-751-359-12
2	449.5	79.8	126	4	US-08-907-146-12
3	434	77.1	229	3	US-08-751-359-22
4	434	77.1	229	4	US-08-907-146-22
5	426.5	75.8	126	3	US-08-751-359-11
6	426.5	75.8	126	4	US-08-907-146-11
7	426	75.7	125	3	US-08-751-359-13
8	426	75.7	125	4	US-08-907-146-13
9	423.5	75.2	124	3	US-08-751-359-14
10	423.5	75.2	124	4	US-08-907-146-14
11	326.5	58.0	108	4	US-09-025-769B-20
12	318	56.5	111	3	US-08-983-607-35
13	309	54.9	109	3	US-09-157-370-5
14	305	54.2	110	1	US-08-199-911-2
15	305	54.2	114	3	US-09-240-274-62
16	304	54.0	112	4	US-09-025-769B-18
17	304	54.0	234	4	US-09-372-425A-4
18	303.5	53.9	143	2	US-08-345-321-8
19	301	53.5	108	1	US-08-360-125-12
20	301	53.5	108	2	US-08-450-578-12
21	301	53.5	108	2	US-09-017-628-12
22	301	53.5	108	2	US-09-014-880-12
23	301	53.3	108	4	US-08-450-363-12
24	300	53.3	109	1	US-08-478-039-91
25	300	53.3	109	1	US-08-476-349A-91
26	300	53.3	111	2	US-08-958-201-12
27	300	53.3	235	3	US-09-049-672A-10

28	298.5	53.0	112	3	US-08-983-607-31	Sequence 31, Appl
29	297	52.8	245	4	US-10-039-785-47	Sequence 47, Appl
30	296	52.6	111	2	US-08-958-201-14	Sequence 14, Appl
31	296	52.6	112	4	US-09-025-769B-19	Sequence 19, Appl
32	295	52.4	113	1	US-08-211-202-112	Sequence 112, Appl
33	295	52.4	245	4	US-10-039-785-45	Sequence 45, Appl
34	294	52.2	109	3	US-09-240-274-61	Sequence 61, Appl
35	294	52.2	111	2	US-08-665-202-43	Sequence 43, Appl
36	294	52.2	111	4	US-09-315-574-43	Sequence 43, Appl
37	294	52.2	245	4	US-10-039-785-43	Sequence 43, Appl
38	293.5	52.1	110	3	US-09-240-274-63	Sequence 63, Appl
39	293	52.0	111	2	US-08-665-202-36	Sequence 36, Appl
40	293	52.0	111	4	US-09-315-574-36	Sequence 36, Appl
41	293	52.0	234	3	US-08-487-550-2	Sequence 2, Appli
42	293	52.0	234	4	US-09-526-098-2	Sequence 2, Appli
43	293	52.0	258	2	US-08-665-202-5	Sequence 5, Appli
44	293	52.0	258	4	US-09-315-574-5	Sequence 5, Appli
45	293	52.0	262	4	US-09-069-821-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-751-359-12  
; Sequence 12, Application US/08751359  
; Patent No. 6143559  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/751,359  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 510  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-751-359-12

Query Match 79.8%; Score 449.5; DB 3; Length 126;  
Best Local Similarity 82.7%; Pred. No. 4.9e-35;  
Matches 91; Conservative 6; Mismatches 6; Indels 7; Gaps 2;  
QY 1 ALTOPSSVSANPGETVKITCSGGSVAGSYVYGYOQKAPASAPVTVIYDNTNPSNIPS 60  
|||||  
DB 22 ALTOPSSVSANPGETVKITCSG-----GSMYGYOQKAPGAPVTTLIYNSQRPDIIPS 76  
|||||

QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108  
 Db 77 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 126

RESULT 2

US-08-907-146-12  
 ; Sequence 12, Application US/08907146  
 ; Patent No. 6316600  
 ; GENERAL INFORMATION:

APPLICANT: Michael, Nancy M  
 APPLICANT: Accavitti, Marianne  
 APPLICANT: Thompson, Craig B  
 TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/907,146  
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/751,359

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARSB:504

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 12:

LENGTH: 126 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-907-146-12

Query Match 79.8%; Score 449.5; DB 4; Length 126;

Best Local Similarity 82.7%; Pred. No. 4.9e-35;

Matches 91; Conservative 6; Mismatches 6; Indels 7; Gaps 2;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60

Db 22 ALTPSSVSANPGETVKITCSG-----GSMYGYGQKAPASAPVTIYNSQRPDIPS 76

QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108

Db 77 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 126

RESULT 3

US-08-751-359-22

; Sequence 22, Application US/08751359

; Patent No. 6143559

; GENERAL INFORMATION:

APPLICANT: Michael, Nancy M

APPLICANT: Accavitti, Marianne

APPLICANT: Thompson, Craig B

TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/907,146

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/751,359

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARSB:504

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 12:

LENGTH: 126 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-907-146-12

Query Match 79.8%; Score 449.5; DB 4; Length 126;

Best Local Similarity 82.7%; Pred. No. 4.9e-35;

Matches 91; Conservative 6; Mismatches 6; Indels 7; Gaps 2;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60

Db 22 ALTPSSVSANPGETVKITCSG-----GSMYGYGQKAPASAPVTIYNSQRPDIPS 76

QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108

Db 77 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 126

US-08-907-146-22

; Sequence 22, Application US/08907146

; Patent No. 6316600

; GENERAL INFORMATION:

APPLICANT: Michael, Nancy M

APPLICANT: Accavitti, Marianne

APPLICANT: Thompson, Craig B

TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 25

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COMPUTER: IBM PC compatible

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SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/907,146

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/751,359

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARSB:504

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 22:

LENGTH: 229 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-751-359-22

Query Match 77.1%; Score 434; DB 3; Length 229;

Best Local Similarity 82.6%; Pred. No. 2.7e-33;

Matches 90; Conservative 2; Mismatches 11; Indels 6; Gaps 2;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60

Db 22 ALTPSSVSANPGETVKITCSGDRS-----YGYGQKAPASAPVTIYDNTNRPSDIPS 76

QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108

Db 77 RFGSKSGSTATITITGVQADDEAVYCGSADSSSTAGIFGAGTTLTVL 125

US-08-907-146-22

; Sequence 22, Application US/08907146

; Patent No. 6316600

; GENERAL INFORMATION:

APPLICANT: Michael, Nancy M

APPLICANT: Accavitti, Marianne

APPLICANT: Thompson, Craig B

TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 25

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STATE: Texas

COUNTRY: USA

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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

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CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/751,359

FILING DATE:

ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARSB:504

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INFORMATION FOR SEQ ID NO: 22:

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STRANDEDNESS:

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Query Match 77.1%; Score 434; DB 3; Length 229;

Best Local Similarity 82.6%; Pred. No. 2.7e-33;

Matches 90; Conservative 2; Mismatches 11; Indels 6; Gaps 2;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60

Db 22 ALTPSSVSANPGETVKITCSGDRS-----YGYGQKAPASAPVTIYDNTNRPSDIPS 76

QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108

Db 77 RFGSKSGSTATITITGVQADDEAVYCGSADSSSTAGIFGAGTTLTVL 125

US-08-907-146-22

; Sequence 22, Application US/08907146

; Patent No. 6316600

; GENERAL INFORMATION:

APPLICANT: Michael, Nancy M

APPLICANT: Accavitti, Marianne

APPLICANT: Thompson, Craig B

TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 25

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SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/907,146

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/751,359

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: ARSB:504

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

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STRANDEDNESS:

TOPOLOGY: linear

US-08-751-359-22

Query Match 77.1%; Score 434; DB 3; Length 229;

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QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYGQKAPASAPVTIYDNTNRPSNIPS 60

Db 22 ALTPSSVSANPGETVKITCSGDRS-----YGYGQKAPASAPVTIYDNTNRPSDIPS 76

QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFDSS--YVGILGAGTTLTVL 108

Db 77 RFGSKSGSTATITITGVQADDEAVYCGSADSSSTAGIFGAGTTLTVL 125

US-08-907-146-22

; Sequence 22, Application US/08907146

; Patent No. 6316600

; GENERAL INFORMATION:

APPLICANT: Michael, Nancy M

APPLICANT: Accavitti, Marianne

APPLICANT: Thompson, Craig B

TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN</



APPLICATION NUMBER: 08/751,359  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 229 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-907-146-22

Query Match 77.1%; Score 434; DB 4; Length 229;  
Best Local Similarity 82.6%; Pred. No. 2.7e-33;  
Matches 90; Conservative 2; Mismatches 11; Indels 6; Gaps 2;

QY 1 ALTQPSVSNPGETVKITCSGGSYAGSYGYGYYQOKAPASAPVTVIYDNTNRPSNIPS 60  
DB 22 ALTQPSVSNPGETVKITCSGDRS-----YGYGYYQOKAPASAPVTVIYDNTNRPSDIPS 76  
QY 61 RFGSLSGSTNTLTITGVQVDEAVYCGSFD-SSYVGIILGAGTTLTVL 108  
DB 77 RFGSKSGSTATLTITGVQADDEAVYCGSADSSSTAGIFGAGTTLTVL 125

RESULT 5  
US-08-751-359-11  
Sequence 11, Application US/08751359  
Patent No. 6143559  
GENERAL INFORMATION:  
APPLICANT: Michael, Nancy M  
APPLICANT: Accavitti, Marianne  
APPLICANT: Thompson, Craig B  
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,359  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 510

ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-751-359-11

Query Match 75.8%; Score 426.5; DB 3; Length 126;

Best Local Similarity 80.0%; Pred. No. 6.9e-33;  
Matches 88; Conservative 2; Mismatches 13; Indels 7; Gaps 2;  
QY 1 ALTQPSVSNPGETVKITCSGGSYAGSYGYGYYQOKAPASAPVTVIYDNTNRPSNIPS 60  
DB 22 ALTQPSVSNPGETVKITCSGDS-----YGYGYYQOKAPASAPVTVIYDNTNRPSNIPS 76  
QY 61 RFGSLSGSTNTLTITGVQVDEAVYCGSFDSSVY--GILGAGTTLTVL 108  
DB 77 RFGSKSGSTATLTITGVRADNAVYCYCASTDSSSTAGIFGAGTTLTVL 126

RESULT 6  
US-08-907-146-11  
Sequence 11, Application US/08907146  
Patent No. 6316600  
GENERAL INFORMATION:  
APPLICANT: Michael, Nancy M  
APPLICANT: Accavitti, Marianne  
APPLICANT: Thompson, Craig B  
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/907,146  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/751,359  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-907-146-11

Query Match 75.8%; Score 426.5; DB 4; Length 126;  
Best Local Similarity 80.0%; Pred. No. 6.9e-33;  
Matches 88; Conservative 2; Mismatches 13; Indels 7; Gaps 2;  
QY 1 ALTQPSVSNPGETVKITCSGGSYAGSYGYGYYQOKAPASAPVTVIYDNTNRPSNIPS 60  
DB 22 ALTQPSVSNPGETVKITCSGDS-----YGYGYYQOKAPASAPVTVIYDNTNRPSNIPS 76  
QY 61 RFGSLSGSTNTLTITGVQVDEAVYCGSFDSSVY--GILGAGTTLTVL 108  
DB 77 RFGSKSGSTATLTITGVRADNAVYCYCASTDSSSTAGIFGAGTTLTVL 126

RESULT 7  
US-08-751-359-13  
Sequence 13, Application US/08751359

Patent No. 6143559  
GENERAL INFORMATION:  
APPLICANT: Michael, Nancy M  
APPLICANT: Accavitti, Marianne  
APPLICANT: Thompson, Craig B  
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,359  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 510  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-751-359-13

Query Match 75.7%; Score 426; DB 3; Length 125;  
Best Local Similarity 80.6%; Pred. No. 7.7e-33;  
Matches 87; Conservative 4; Mismatches 11; Indels 6; Gaps 2;  
QY 2 LTQPSVSANPGTAVKTCGGGVSAGSYGYGYQKAPASAPVTYVDNTRPSNIPSR 61  
Db 23 LIQPTSVSANPGTAVKTCGSG-----DTIYIGWYQKAPGSAFVTYVDNTRPSNIPSR 77  
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFD-SSYVGILGAGTTTLVL 108  
Db 78 FSGSLSGSTNTLTITGVQVEDEAVYFCANADSSSTAGIFGAGTTTLVL 125  
RESULT 8  
US-08-907-146-13  
Sequence 13, Application US/08907146  
Patent No. 6316600  
GENERAL INFORMATION:  
APPLICANT: Michael, Nancy M  
APPLICANT: Accavitti, Marianne  
APPLICANT: Thompson, Craig B  
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/907,146  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/751,359  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-907-146-13  
Query Match 75.7%; Score 426; DB 4; Length 125;  
Best Local Similarity 80.6%; Pred. No. 7.7e-33;  
Matches 87; Conservative 4; Mismatches 11; Indels 6; Gaps 2;  
QY 2 LTQPSVSANPGTAVKTCGGGVSAGSYGYGYQKAPASAPVTYVDNTRPSNIPSR 61  
Db 23 LIQPTSVSANPGTAVKTCGSG-----DTIYIGWYQKAPGSAFVTYVDNTRPSNIPSR 77  
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFD-SSYVGILGAGTTTLVL 108  
Db 78 FSGSLSGSTNTLTITGVQVEDEAVYFCANADSSSTAGIFGAGTTTLVL 125  
RESULT 9  
US-08-751-359-14  
Sequence 14, Application US/08751359  
Patent No. 6143559  
GENERAL INFORMATION:  
APPLICANT: Michael, Nancy M  
APPLICANT: Accavitti, Marianne  
APPLICANT: Thompson, Craig B  
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,359  
FILING DATE: Concurrently Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:

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; LENGTH: 124 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-751-359-14

Query Match 75.2%; Score 423.5; DB 3; Length 124;  
Best Local Similarity 76.9%; Pred. No. 1.3e-32;  
Matches 83; Conservative 6; Mismatches 14; Indels 5; Gaps 1;  
  
QY 1 ALTOPSSVSANPGETVKITCSGGSYAGSYGYQOKAPASAPVTIYDNTNRPNSIPS 60  
DQ 22 ALTOPASVSANPGETVEITCSGDSS-----YGYQOKAPGAPVTIYDNTNRPNSIPS 76  
  
QY 61 RFGSLSGSTNTLTITGVQVDEAVYCGSFDSSYVGLGAGTTLTVL 108  
DQ 77 RFGSKSGSTALTITGVRADEGIYCASTDSSSTAFAFGAGTTLTVL 124

RESULT 10  
US-08-907-146-14  
; Sequence 14, Application US/08907146  
; Patent No. 6316600  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/907,146  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/751,359  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-907-146-14

Query Match 75.2%; Score 423.5; DB 4; Length 124;  
Best Local Similarity 76.9%; Pred. No. 1.3e-32;  
Matches 83; Conservative 6; Mismatches 14; Indels 5; Gaps 1;  
  
QY 1 ALTOPSSVSANPGETVKITCSGGSYAGSYGYQOKAPASAPVTIYDNTNRPNSIPS 60  
DQ 22 ALTOPASVSANPGETVEITCSGDSS-----YGYQOKAPGAPVTIYDNTNRPNSIPS 76  
  
QY 61 RFGSLSGSTNTLTITGVQVDEAVYCGSFDSSYVGLGAGTTLTVL 108

Db 77 RFGSKSGSTALTITGVRADEGIYCASTDSSSTAFAFGAGTTLTVL 124  
  
RESULT 11  
US-09-025-769B-20  
; Sequence 20, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-20

Query Match 58.0%; Score 326.5; DB 4; Length 108;  
Best Local Similarity 64.5%; Pred. No. 1.3e-23;  
Matches 69; Conservative 7; Mismatches 28; Indels 3; Gaps 2;  
  
QY 2 LTQPPSSVSANPGETVKITCSGGSYAGSYGYQOKAPASAPVTIYDNTNRPNSIPS 61  
DQ 3 LTQPPSSVSANPGETVKITCSGDSS--LGSKYASWYQOK-PQAPVLVIYDDNKRPSGIPER 59  
  
QY 62 FSGSLSGSTNTLTITGVQVDEAVYCGSFDSSYVGLGAGTTLTVL 108  
DQ 60 FSGNSGNTATLTISGVAEDEADYVCGSWDSSGNVVFSGGKTLTVL 106

RESULT 12  
US-08-983-607-35  
; Sequence 35, Application US/08983607  
; Patent No. 6140470  
; GENERAL INFORMATION:  
; APPLICANT: Alan Garen  
; APPLICANT: Xiaohong Cai  
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-  
; TITLE OF INVENTION: bodies

```

; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scfv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V373
; FEATURE:
; NAME/KEY: light chain
; US-08-983-607-35

Query Match 56.5%; Score 318; DB 3; Length 111;
Best Local Similarity 59.6%; Pred. No. 8.1e-23;
Matches 65; Conservative 12; Mismatches 30; Indels 2; Gaps 2;
QY 1 ALTOPSSVSANPGETVKITCGSGSYAGSYGGYQKAPASAPVTVIYDNTNRPSPNPS 60
Db 3 ALTOPPSVSAPGQKVTISCGSSNGNNTVSWY-QRLPGTAPKLLIYENKRPSPGPD 61
QY 61 RFGSLSGSTNLTITGVQVEDEAVYCGSFDSSVVG-ILGAGTTLVL 108
Db 62 RFGSKSGTSATLITGLQAEDEAGYQCQSDSSLSGVTGKTLVL 110

RESULT 13
US-09-157-370-5
; Sequence 5, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21

; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scfv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V373
; FEATURE:
; NAME/KEY: light chain
; US-08-983-607-35

Query Match 54.9%; Score 309; DB 3; Length 109;
Best Local Similarity 61.7%; Pred. No. 5.5e-22;
Matches 66; Conservative 10; Mismatches 27; Indels 4; Gaps 3;
QY 2 LTQPSVSANPGETVKITCGSGSYAGSYGGYQKAPASAPVTVIYDNTNRPSPNPS 61
Db 4 LTQPPSVSVSPGQTVTISCGDS--LGIGYVSWYQK-PGQAPKLVYIDNKRPSGIPDR 60
QY 62 FSGSLSGSTNLTITGVQVEDEAVYCGSFDSSVVG-ILGAGTTLVL 108
Db 61 FSGSKSGTSATLITGLQAEDEAGYQCQSDSSV-VFGGTTKLVL 106

RESULT 14
US-08-199-911-2
; Sequence 2, Application US/08199911
; Patent No. 5495002
; GENERAL INFORMATION:
; APPLICANT: Kofrin, Barry J.
; APPLICANT: Haspel, Martin V.
; TITLE OF INVENTION: Tumor Associated Monoclonal Antibody
; TITLE OF INVENTION: 123AV16
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AKZO NOBEL
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,911
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,517
; FILING DATE: 21-MAY-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/636,179
; FILING DATE: 31-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/302,155
; FILING DATE: 25-JAN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/697,078
; FILING DATE: 31-JAN-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/575,533
; FILING DATE: 31-JAN-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:10:30 ; Search time 20.0625 Seconds  
(without alignments)  
739.130 Million cell updates/sec

Title: US-10-083-424A-26  
Perfect score: 563  
Sequence: 1 ALTOPSSVSANPGETVKITC.....GSPDSSVYVILGAGTTTLVL 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues  
Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
1	563	100.0	108	15	US-10-083-424-26
2	418.5	74.3	105	15	US-10-083-424-32
3	401	71.2	108	15	US-10-083-424-30
4	394	70.0	104	15	US-10-083-424-28
5	384.5	68.3	104	15	US-10-083-424-40
6	318	56.5	249	11	US-09-880-748-1312
7	315	56.0	251	11	US-09-880-748-1556
8	315	56.0	251	11	US-09-880-748-1840
9	312	55.4	106	15	US-10-269-805-8
10	312	55.4	255	11	US-09-880-748-1156
11	310	55.1	258	11	US-09-880-748-1260
12	309.5	55.0	111	15	US-10-269-805-54
13	309.5	55.0	217	11	US-09-972-656-88
14	308	54.9	123	15	US-10-153-437-6
15	308	54.7	109	15	US-10-001-934-44

16	308	54.7	245	15	US-10-151-882-15	Sequence 15, Appl
17	308	54.7	248	11	US-09-880-748-861	Sequence 861, App
18	308	54.7	258	11	US-09-880-748-1029	Sequence 1029, Ap
19	307.5	54.6	111	15	US-10-269-805-6	Sequence 6, Appli
20	307	54.5	110	15	US-10-269-805-58	Sequence 58, Appli
21	307	54.5	111	15	US-10-199-908-4	Sequence 4, Appli
22	306.5	54.4	245	11	US-09-880-748-1864	Sequence 1864, Ap
23	306.5	54.4	252	11	US-09-880-748-1549	Sequence 1549, Ap
24	306.5	54.4	252	11	US-09-880-748-1992	Sequence 1992, Ap
25	306	54.4	246	11	US-09-880-748-2077	Sequence 2077, Ap
26	306	54.4	253	11	US-09-880-748-1859	Sequence 1859, Ap
27	306	54.4	256	11	US-09-880-748-1015	Sequence 1015, Ap
28	305.5	54.3	253	11	US-09-880-748-1375	Sequence 1375, Ap
29	305	54.2	109	15	US-10-001-934-50	Sequence 50, Appl
30	305	54.2	114	11	US-09-848-798-62	Sequence 62, Appl
31	305	54.2	248	11	US-09-880-748-1995	Sequence 1995, Ap
32	305	54.2	249	11	US-09-880-748-1572	Sequence 1572, Ap
33	305	54.2	249	11	US-09-880-748-1373	Sequence 1373, Ap
34	305	54.2	250	11	US-09-880-748-1565	Sequence 1565, Ap
35	305	54.2	250	11	US-09-880-748-1566	Sequence 1566, Ap
36	305	54.2	252	11	US-09-880-748-1208	Sequence 1208, Ap
37	304	54.0	109	15	US-10-001-934-52	Sequence 52, Appl
38	304	54.0	254	11	US-09-880-748-1139	Sequence 1139, Ap
39	304	54.0	255	11	US-09-880-748-857	Sequence 857, App
40	303.5	53.9	252	11	US-09-880-748-988	Sequence 988, App
41	303.5	53.9	253	11	US-09-880-748-909	Sequence 909, App
42	303.5	53.9	253	11	US-09-880-748-1125	Sequence 1125, Ap
43	303.5	53.9	256	11	US-09-880-748-1301	Sequence 1301, Ap
44	303	53.8	112	15	US-10-269-805-10	Sequence 10, Appl
45	303	53.8	251	11	US-09-880-748-1538	Sequence 1538, Ap

ALIGNMENTS

RESULT 1

US-10-083-424-26  
; Sequence 26, Application US/10083424  
; Publication No. US20030104497A1  
; GENERAL INFORMATION:  
; APPLICANT: Avicore Biotechnology Institute Inc.  
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Eimeria spp. Respo  
; FILE REFERENCE: for Coccidiosis  
; FILE REFERENCE: AVICORE-USA-1  
; CURRENT APPLICATION NUMBER: US/10/083,424  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: KR 2001-52934  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 26  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: chicken hybridoma cell line 2-1  
US-10-083-424-26

Query Match	100.0%	Score 563;	DB 15;	Length 108;
Best Local Similarity	100.0%	Pred No. 5	6e-48;	
Matches 108;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ALTOPSSVSANPGETVKITC	SGGSGSYAGSYGYGWYQOKAPASAPVT	VIYDNTNRPSNIPS 60
Db	1	ALTOPSSVSANPGETVKITC	SGGSGSYAGSYGYGWYQOKAPASAPVT	VIYDNTNRPSNIPS 60
Qy	61	RFGSLSGSTNTLTITG	VQVDEAVYVCGSFDSSVYVILGAGTTTLVL	108
Db	61	RFGSLSGSTNTLTITG	VQVDEAVYVCGSFDSSVYVILGAGTTTLVL	108

RESULT 2

US-10-083-424-32  
; Sequence 32, Application US/10083424  
; Publication No. US20030104497A1





RESULT 8  
US-09-880-748-1840  
; Sequence 1840, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION;

RESULT 10  
US-09-880-748-1156  
; Sequence 1156, Application US/09880748  
; Publication No. US20030059937A1

Query Match	55.1%	Score 310;	DB 11;	Length 258;
Best local similarity	59.3%;	Pred. NO. 9.8e-23;		
Matches	64;	Conservative 12;	Mismatches 30;	Indels 2;
Gaps	2;			
Qy	2	LTPQSVSNPGETVATCTCGSGYAGSYGYGWYQKAPASAPVTVIYDNTNRPSNIPRS	61	
Db	151	LQTQPPVSAAPQKVTICSGSSSSNTGNNVSVYQQ-LFGTAPKLLIYDNNKRKPSGIPDR	209	

RESULT 14  
US-10-153-437-6

; Sequence 6, Application US/10153437  
 ; Publication No. US20030124631A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pier, Gerald B.  
 ; APPLICANT: Preston, Michael J.  
 ; APPLICANT: Cavacini, Lisa  
 ; APPLICANT: Posner, Marshall  
 ; TITLE OF INVENTION: P. aeruginosa Mucoic Exopolysaccharide Specific Binding Peptides  
 ; FILE REFERENCE: B00801/70250  
 ; CURRENT APPLICATION NUMBER: US/10/153,437  
 ; CURRENT FILING DATE: 2002-05-21  
 ; PRIOR APPLICATION NUMBER: US 60/292,365  
 ; PRIOR FILING DATE: 2001-05-21  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 123  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-153-437-6

Query Match 54.9%; Score 309; DB 15; Length 123;  
 Best Local Similarity 58.3%; Pred. No. 5.2e-23;  
 Matches 63; Conservative 14; Mismatches 29; Indels 2; Gaps 2;  
 QY 2 LTQPSVSANPGETVKITCGSGSYAGSYGYGWTQKAPASAPVTVIYDNTNRPSNIPSR 61  
 Db 16 LTQPPSVSAPGQRTVISCSSGSLGNFVSWYQQ-LPGAAPRLIYDNDKRPSPGIPDR 74  
 QY 62 FSGSLSGSTNTLTITGQVDEAVYYCGSFDSYVVG-ILGAGTTLTVL 108  
 Db 75 FSGSKSGTSATLITGLQGTDEADYYCGTWDSSLTAYVFGSGTKTVL 122

RESULT 15  
 US-10-001-934-44  
 ; Sequence 44, Application US/10001934  
 ; Publication No. US20030032782A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAGY, ZOLTAN  
 ; TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE  
 ; KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS  
 ; FILE REFERENCE: GPCG-P01-003  
 ; CURRENT APPLICATION NUMBER: US/10/001,934  
 ; CURRENT FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 44  
 ; LENGTH: 109  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-001-934-44

Query Match 54.7%; Score 308; DB 15; Length 109;  
 Best Local Similarity 57.9%; Pred. No. 5.7e-23;  
 Matches 62; Conservative 13; Mismatches 30; Indels 2; Gaps 2;  
 QY 2 LTQPSVSANPGETVKITCGSGSYAGSYGYGWTQKAPASAPVTVIYDNTNRPSNIPSR 61  
 Db 4 LTQPPSVSAPGQRTVISCSSGSLGNFVSWYQQ-LPGAAPRLIYDNDKRPSPGIPDR 62  
 QY 62 FSGSLSGSTNTLTITGQVDEAVYYCGSFDSYVVG-ILGAGTTLTVL 108  
 Db 63 FSGSKSGTSATLITGLQGTDEADYYCGSYDILT-MGVFGGKTLTVL 108

Search completed: September 3, 2003, 12:53:16  
 Job time : 21.0625 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 12:02:19 ; Search time 24.4688 Seconds  
(without alignments)  
1138.991 Million cell updates/sec

Title: US-10-083-424A-26

Perfect score: 563

Sequence: 1 ALTOPSSVSANPGETVKITC.....GSFSSVYGILGAGTTLTVL 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	305	54.2	110	4	Q8TE63
2	300	53.3	233	4	Q8TEC9
3	297.5	52.8	112	4	Q96JDI
4	296.5	52.7	107	4	Q9UL82
5	295	52.4	237	4	Q8WUK4
6	294	52.2	233	4	Q8NSF4
7	292	51.9	116	4	Q96JDO
8	290	51.5	107	4	Q9NSD6
9	289	51.3	237	4	Q8WTRU6
10	288.5	51.2	234	4	Q8NS355
11	288.5	51.2	236	4	Q96E61
12	288	51.2	112	4	Q96JDI
13	275.5	48.9	236	4	Q8NEJ1
14	267	47.4	101	4	Q8IZD8
15	256.5	45.6	108	4	Q96SB0
16	242	43.0	233	4	Q96I69

17	237	42.1	235	11	Q99M11	Q99M11	mus	musculus
18	234	41.6	113	11	O8CGS1	O8CGS1	mus	musculus
19	223	39.6	114	11	O8K1F1	O8K1F1	mus	musculus
20	222	39.4	112	11	O8K1F3	O8K1F3	mus	musculus
21	221	39.3	106	5	Q9U410	Q9U410	schistosoma	
22	221	39.3	134	11	O8VDD0	O8VDD0	mus	musculus
23	220	39.1	97	11	O9ET13	O9ET13	mus	musculus
24	218	38.7	109	11	O9UL76	O9UL76	mus	musculus
25	215	38.2	112	11	O8K1F2	O8K1F2	mus	musculus
26	212	37.7	107	4	O9UL81	O9UL81	homo	sapien
27	211.5	37.6	129	11	O8VDE2	O8VDE2	mus	musculus
28	206.5	36.7	108	4	O9UL70	O9UL70	homo	sapien
29	206	36.6	109	4	O9UL78	O9UL78	homo	sapien
30	205.5	36.5	108	4	O9UL77	O9UL77	homo	sapien
31	205	36.4	112	11	O8K1F0	O8K1F0	mus	musculus
32	204	36.2	101	11	O9UL78	O9UL78	mus	musculus
33	204	36.2	107	4	Q96SA9	Q96SA9	homo	sapien
34	198	35.2	109	4	O9UL86	O9UL86	homo	sapien
35	194.5	34.5	234	4	O8NEK1	O8NEK1	homo	sapien
36	192.5	34.2	108	4	O9UL83	O9UL83	homo	sapien
37	192	34.1	109	4	O9UL85	O9UL85	homo	sapien
38	192	34.1	235	11	O9UL82	O9UL82	mus	musculus
39	190.5	33.8	109	6	Q9N0W5	Q9N0W5	oryctolagus	
40	190.5	33.8	214	11	O9RIA5	O9RIA5	mus	musculus
41	190.5	33.8	240	4	Q8WUK3	Q8WUK3	homo	sapien
42	188.5	33.5	108	4	O9UL79	O9UL79	homo	sapien
43	184.5	32.8	298	11	O9QYF0	O9QYF0	mus	musculus
44	183.5	32.6	109	11	O920E6	O920E6	mus	musculus
45	180.5	32.1	234	11	O8R062	O8R062	mus	musculus

#### ALIGNMENTS

RESULT 1

Q8TE63 PRELIMINARY; PRT; 110 AA.  
ID Q8TE63  
AC Q8TE63;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95007525; PubMed=7923137;  
RA Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;  
RT "Establishment, molecular rescue, and expression of 123AV16-1, a tumor-reactive human monoclonal antibody.";  
RL Cancer Res. 54:5178-5185(1994).  
DR EMBL; L33985; AAL68704.1; -  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 110  
SQ SEQUENCE 110 AA; 599D1628F8F5437C CRC64;

Query Match 54.2%; Score 305; DB 4; Length 110;  
Best Local Similarity 56.9%; Pred. No. 3.le-22;  
Matches 62; Conservative 14; Mismatches 31; Indels 2; Gaps 2;  
QY 1 ALTOPSSVSANPGETVKITCSGGSYAGSYGYGQKAPASAPVTYIDNTRPSNIPS 60  
Db 3 ALTOPSSVSANPGQKVTISCSNINNFVSWYQQ-FPGAPKLLIYDNNKRPSSGVPD 61  
QY 61 RFSGSLSGSTNTLTITGVQVEDEAVYCGSFSSY-VGILGAGTTLTVL 108

```

Best Local Similarity 53.2%; Pred. No. 1.7e-21;
Matches 58; Conservative 18; Mismatches 30; Indels 3; Gaps 2;

QY      2 LTQPSSVSANPETVKITCSGGSGAGSYGYGKQKAPASAPVTVIYDNTNRPSNIPSR 61
        ||||| :||:||||:|:|:| | ||||| :||:||||:| | | | |
Db       4 LTQPHSVSESPGKTITISCTRSSGIASNVMYQQQR-PGSAPTIIYEDNQRPSPGVDR 62
        ||||| :||:||||:|:|:| | ||||| :||:||||:| | | | |

QY      62 FSGSLSGSTN--TITIGVQVEDEAVYYCGSFDSSYVGILGAGTTLTVL 108
        ||||| :||:||||:|:|:| | ||||| :||:||||:| | | | |
Db       63 FSGSIDSSNSASLTISGLKTEADAYYCQSDSNYNALFGGGTQLTVL 111
        ||||| :||:||||:|:~|~| | ||||| :||:||||:| | | | |

RESULT 4
Q9UL82    PRELIMINARY;          PRT;   107 AA.
ID Q9UL82
AC Q9UL82
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035032; AAD56268.1; -
DR HSSP; F01703; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT TER 107
SQ SEQUENCE 107 AA; 11445 MW; 52FOCCIAB26821DC CRC64;

Query Match
Best Local Similarity 52.7%; Score 296.5; DB 4; Length 107;
Matches 62; Conservative 11; Mismatches 31; Indels 3; Gaps 2;

QY      2 LTQPSSVSANPETVKITCSGGSGAGSYGYGKQKAPASAPVTVIYDNTNRPSNIPSR 61
        ||||| :||:||||:|:|:| | ||||| :||:||||:| | | | |
Db       4 LTQPHSVSESPGQTARTCS--GDLLAKKYARWFOOK-PCQAPILVFNDTERPSGIPR 60
        ||||| :||:||||:|:|:| | ||||| :||:||||:| | | | |

QY      62 FSGSLSGSTNLTITIGVQVEDEAVYYCGSFDSSYVGILGAGTTLTVL 108
        ||||| :||:||||:|:~|~| | ||||| :||:||||:| | | | |
Db       61 FSGSSSCTTTLTISGAQVEADAYCYCASDNNGRVFGGGTKLTVL 107
        ||||| :||:||||:|:~|~| | ||||| :||:||||:| | | | |

RESULT 5
Q8WUK4    PRELIMINARY;          PRT;   237 AA.
ID Q8WUK4
AC Q8WUK4
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE=Tonsil;
```

```
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020233; AAH20233.1;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 52.4%; Score 295; DB 4; Length 237;
Best Local Similarity 56.4%; Pred. No. 7.3e-21;
Matches 62; Conservative 14; Mismatches 30; Indels 4; Gaps 3;

QY 2 LTQPSVSNAPGETVKITCSGGGAGS-YYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 60
DQ 23 LTQPSVSNAPGETVKITCSGGGAGS-YYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 60
QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYG--ILGAGTTTLTVL 108
DQ 82 RFGSGKTSASLAITGLQAEDEADYCYQSDSSLSGFVFGGKTLTVL 131

RESULT 6
ID Q8N5F4 PRELIMINARY; PRT; 233 AA.
AC Q8N5F4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022452; AAH32452.1;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24961 MW; F092CFB6AA6E3A9A CRC64;

Query Match 52.2%; Score 294; DB 4; Length 233;
Best Local Similarity 60.0%; Pred. No. 9e-21;
Matches 66; Conservative 10; Mismatches 26; Indels 8; Gaps 5;

QY 2 LTQPSVSNAPGETVKITCSGGGAGSYYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 61
DQ 23 LTQPSVSNAPGETVKITCSGGGAGSYYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 61
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYG--ILGAGTTTLTVL 108
DQ 80 FSGSSGIVATLTLSGAQVEDEADYCYSDSS--GNHWVFGGKTLTVL 127

RESULT 7
ID Q96JD0 PRELIMINARY; PRT; 116 AA.
AC Q96JD0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020233; AAH20233.1;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

Query Match 52.4%; Score 295; DB 4; Length 237;
Best Local Similarity 56.4%; Pred. No. 7.3e-21;
Matches 62; Conservative 14; Mismatches 30; Indels 4; Gaps 3;

QY 2 LTQPSVSNAPGETVKITCSGGGAGS-YYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 60
DQ 23 LTQPSVSNAPGETVKITCSGGGAGS-YYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 60
QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYG--ILGAGTTTLTVL 108
DQ 82 RFGSGKTSASLAITGLQAEDEADYCYQSDSSLSGFVFGGKTLTVL 131

RESULT 6
ID Q8N5F4 PRELIMINARY; PRT; 233 AA.
AC Q8N5F4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022452; AAH32452.1;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24961 MW; F092CFB6AA6E3A9A CRC64;

Query Match 52.2%; Score 294; DB 4; Length 233;
Best Local Similarity 60.0%; Pred. No. 9e-21;
Matches 66; Conservative 10; Mismatches 26; Indels 8; Gaps 5;

QY 2 LTQPSVSNAPGETVKITCSGGGAGSYYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 61
DQ 23 LTQPSVSNAPGETVKITCSGGGAGSYYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 61
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYG--ILGAGTTTLTVL 108
DQ 80 FSGSSGIVATLTLSGAQVEDEADYCYSDSS--GNHWVFGGKTLTVL 127

RESULT 7
ID Q96JD0 PRELIMINARY; PRT; 116 AA.
AC Q96JD0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
```

```
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Amyloid lambda 6 light chain variable region SAR (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267875; AAK58587.1;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12294 MW; F7B0E9F49FAE369E CRC64;

Query Match 51.9%; Score 292; DB 4; Length 116;
Best Local Similarity 55.0%; Pred. No. 6e-21;
Matches 61; Conservative 17; Mismatches 27; Indels 6; Gaps 4;

QY 2 LTQPSVSNAPGETVKITCSGGGAGSYYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 61
DQ 4 LTQPHSVSESPGKTVTISCTSGSGSIATNYQVQYQLR-FGSAPVTVIYDNTNRPSPNIPS 62
QY 62 FSGSLSGSTN--TLTITGVQVEDEAVYCGSFSSVYG--ILGAGTTTLTVL 108
DQ 63 FSGSIDSSNSASLTISGLKTEADYCYQSDSS-IGNVIFGGKTLTVL 112

RESULT 8
ID Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RA Hohmann A.;
RT "Autoimmunity.";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; LA3092; AAA69746.2;
DR HSSP; P01709; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 51.5%; Score 290; DB 4; Length 107;
Best Local Similarity 60.2%; Pred. No. 8.6e-21;
Matches 65; Conservative 5; Mismatches 34; Indels 4; Gaps 3;

QY 2 LTQPSVSNAPGETVKITCSGGGAGSYYGYWYQOKAPASAPVTVIYDNTNRPSPNIPS 61
DQ 2 LTQDPVVSVALGQTVRITCQGDG--LRSYYASWYQOK-PGQAPVLVIYGNRPSGIPDR 58
```

RESULT 10	
QBN355	PRELIMINARY; PRT; 234 AA.
ID	QBN355
AC	QBN355;
DT	01-OCT-2002 (TREMBLrel. 22; Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RA	Strausberg R.;
RL	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC028090; AAH28090.1; -
DR	InterPro; IPR003599; Ig_
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig_cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PF00047; Ig_2.
DR	SMART; SM00409; IG1. 2.
DR	SMART; SM00407; IGcl; 1.

```

SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match
Best Local Similarity 51.2%; Score 288.5; DB 4; Length 236;
Matches 60; Conservative 15; Mismatches 31; Indels 3; Gaps 3;

QY 2 LTDPSSVSANGENVKITCSGGSGYAGS-YYIGWYQOKAPASAPVTVIYDNTNRPSNIPS 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
23 LAQPPSPVSGAPQGTIVTISCTSSNIGAGYAVHWYQ-FPCAAPKVLIYIGNRPSGVPD 81
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 RFSGSLSGSTNLTITGQVDEAVVYCGSFDSSYYQ-ILGAGTTTLVL 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
82 RFSGSKGTSASLAITGLQADEADYYCYQSYDGLSGSVEFGAGTKVTVL 130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
Q96JDD
ID Q96JDD PRELIMINARY; PRT: 112 AA.
AC Q96JDD;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DS Anyloidd lambda 6 light chain variable region NEG (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]

```

```

Query Match          51.2%; Score 288.5; DB 4; Length 236;
Best Local Similarity 55.0%; Pred. No. 3.1e-20;
Matches 60; Conservative 15; Mismatches 31; Indels 3;

2  LTQPSYSVANGPEVVKITCSGGGSYAGS-YTYGWYQOKAPASAPATVLYDNTN
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
23 LAQPPSVSGAPQGTVTICTSGSTNIGAYVHVYQQ-FPGAAPKVLIIYGNFN
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 RFSGSLSGSTNLTITGQVDEAVYYCGSFDSSVVG-ILGAGTTLTFLV 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
82 RFSGSKSGTSASLAIITGLQDEADYTCQSYDGLSGSVFAGGKTVTL 130
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



```
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region NEG.";
RL EMBL; AF267873; AAK59585.1; -;
DR Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267873; AAK59585.1; -;
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E22360B06 CRC64;

Query Match 51.2%; Score 288; DB 4; Length 112;
Best Local Similarity 53.6%; Pred. No. 1.4e-20;
Matches 59; Conservative 16; Mismatches 31; Indels 4; Gaps 3;

QY 2 LTQPSVSNPGETVKITCGGGSYAGSYYYGWYQOKAPASAPVTVIYDNTNRPSPR 61
DB 4 LTQHSVSGSPQRTITSCGSRGRIASNSVQWYQQR-PGSAPNIVMENNORPSGVDP 62

QY 62 FSGSLSGSTN--TLTITGVQVEDEAVYYCGSF-DSSYVGILGAGTTTLTVL 108
DB 63 FSGSIDSSNSASLTISGLMTEDEADYYCQSFDDSTNQGVFGGTRTLTVL 112

RESULT 13
Q8NEJ1 PRELIMINARY; PRT; 236 AA.
AC Q8NEJ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; RAH30984.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 48.9%; Score 275.5; DB 4; Length 236;
Best Local Similarity 52.7%; Pred. No. 5.7e-19;
Matches 58; Conservative 16; Mismatches 31; Indels 5; Gaps 3;

QY 2 LTQPSVSNPGETVKITCGGGSYAGSYYYGWYQOKAPASAPVTVIYDNTNRPSPR 61
DB 23 LTQPPSAGSGPQRTITSCGSRGRIASNSVQWYQQR-VPGTAPKLLIYRNDQRPSPGVDP 81

QY 62 FSGSLSGSTNLTITGVQVEDEAVYYCGSF-DSS---YVGILGAGTTTLTVL 108
DB 82 FSGSKSGTSASLTISGLRSEDEADYYCAAWDDSLSHVH-VFGGTRTLTVL 130
```

```
RESULT 14
Q81ZD8 PRELIMINARY; PRT; 101 AA.
ID Q81ZD8;
AC Q81ZD8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-thyroglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RT "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145444; AAN64328.1; -;
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;

Query Match 47.4%; Score 267; DB 4; Length 101;
Best Local Similarity 54.5%; Pred. No. 1.4e-18;
Matches 55; Conservative 13; Mismatches 31; Indels 2; Gaps 2;

QY 9 SANPGETVKITCGGGSYAGSYYYGWYQOKAPASAPVTVIYDNTNRPSPRSGSLSG 68
DB 1 SAAPGQKVTITSCGSSSNIGKNYVSWYQ-QVGTAPQLIHDTDKRPSGTPDRFSGSQS 59

QY 69 STNTLTITGVQVEDEAVYYCGSFSSVYGCIL-GAGTTTLTVL 108
DB 60 TSATLGTITGLTGDEADYYCGTWTDSLAVFVGKTKLTVL 100

RESULT 15
Q96SB0 PRELIMINARY; PRT; 108 AA.
ID Q96SB0;
AC Q96SB0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-streptococcal/anti-mycosin immunoglobulin lambda light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96394; AAB68783.1; -;
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match 45.6%; Score 256.5; DB 4; Length 108;
Best Local Similarity 51.0%; Pred. No. 1.6e-17;
Matches 50; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 2 LTQPSVSNPGETVKITCGGGSYAGSYYYGWYQOKAPASAPVTVIYDNTNRPSPR 61
```

Db       |||||   ||:|   |:||||   |||   ||||   |:||   |:||||   |||   :|  
4   LTQPPASGTPGQRTISCSSNIGSNVYVYQO-LPGTAPKLLIYRNNQRPSPGVPDR 62  
QY       |||||   ||:|   |:||||   |||   ||||   |:||   |:||||   |||   :|  
62   FSGSLSGSTNTLTITGQVQVEDEAVYCGSFDSSYVGIL 99  
Db       |||||   ||:|   |:||||   |||   ||||   |:||   |:||||   |||   :|  
63   FSGSKGTSASLAISGLRSEDEADYCAAWDDRLSGFM 100

Search completed: September 3, 2003, 12:14:47  
Job time : 25.4688 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:02:54 ; Search time 9.28125 Seconds  
(without alignments)  
1119.054 Million cell updates/sec

Title: US-10-083-424A-26

Perfect score: 563

Sequence: 1 ALTOPSSVSANPGETVKITC.....GSFDDSYVYGLGAGTTTLVL 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	434	77.1	125	2 A31493	Ig light chain pre
2	430	76.4	213	2 A21177	Ig light chain pre
3	419.5	74.5	230	2 S49449	Ig lambda chain
4	403.5	71.7	113	1 L1CHV	Ig lambda chain pr
5	386.5	68.7	97	2 I51216	Ig light chain var
6	317	56.3	235	2 S05270	Ig lambda chain pr
7	313	55.6	111	2 S47009	Ig lambda chain V1
8	311	55.2	111	1 L1HUNG	Ig lambda chain V-
9	307	54.5	130	1 L1HUBL	Ig lambda chain pr
10	306	54.4	131	2 S24321	Ig lambda chain pr
11	302.5	53.7	120	2 S30525	Ig lambda chain V
12	302	53.6	105	2 S49533	Ig lambda chain V
13	301	53.5	119	2 S30526	Ig lambda chain V
14	300	53.3	231	2 S25751	Ig lambda chain -
15	299	53.1	107	1 L4HUL	Ig lambda chain V-
16	299	53.1	111	2 S38497	Ig lambda chain -
17	299	53.1	111	2 S47185	Ig lambda chain -
18	298	52.9	130	2 S09712	Ig lambda chain V
19	297.5	52.8	110	2 S36272	Ig lambda chain V
20	297	52.8	113	2 A29700	Ig lambda chain V
21	295.5	52.5	112	1 L6HUAR	Ig lambda chain V-
22	295	52.4	106	1 L4HUBU	Ig lambda chain V-
23	295	52.4	111	2 S36274	Ig lambda chain V
24	295	52.4	235	2 S25758	Ig lambda chain -
25	294.5	52.3	111	2 S44105	Ig lambda chain V-
26	294	52.2	112	2 S19664	Ig lambda chain V
27	294	52.2	232	2 S25742	Ig lambda chain -
28	294	52.2	235	2 S25759	Ig lambda chain -
29	293.5	52.1	232	2 S25756	Ig lambda chain -

30	293	52.0	108	2 S47184	Ig lambda chain -
31	293	52.0	109	2 S19663	Ig lambda chain V
32	292.5	52.0	131	1 L6HUEB	Ig lambda chain pr
33	292	51.9	108	2 S38498	Ig lambda chain -
34	291.5	51.8	112	2 S31515	Ig lambda chain V
35	291.5	51.8	112	2 S51148	antibody light cha
36	291	51.7	127	2 S70444	Ig lambda chain pr
37	291	51.7	231	2 S25738	Ig lambda chain -
38	290	51.5	109	1 L1HUEP	Ig lambda chain V-
39	290	51.5	111	2 S46397	Ig lambda chain V
40	289.5	51.4	112	2 S46395	Ig lambda chain V
41	289	51.3	111	2 S36263	Ig lambda chain V-
42	288	51.2	111	1 L2HUNI	Ig lambda chain V-
43	287	51.0	111	1 L2HUBH	Ig lambda chain V-
44	287	51.0	111	1 L6HULT	Ig lambda chain V-
45	287	51.0	120	2 S30527	Ig lambda chain V

ALIGNMENTS

RESULT 1

A31493  
Ig light chain precursor V region - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Jul-1989 #sequence\_revision 13-Jul-1989 #text\_change 21-Jan-2000  
C:Accession: A31493  
R:McCormack, W.T.; Tjoelker, L.W.; Carlson, L.M.; Petryniak, B.; Barth, C.F.; Humm  
Cell 56, 785-791, 1989  
A:Title: Chicken IgL gene rearrangement involves deletion of a circular episome a  
A:Reference number: A31493; MUID:89168419; PMID:2493991  
A:Accession: A31493  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-125 <MCC>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:34-105/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 434; DB 2; Length 125;  
Best Local Similarity 82.6%; Pred. No. 3.3e-31;  
Matches 90; Conservative 2; Mismatches 11; Indels 6; Gaps 2;

Qy	1	ALTOPSSVSANPGETVKITCSGGSVAGSYGYQYQKAPASAPVTVIYDNTNRPSNIPS	60
Db	22	ALTOPSSVSANPGETVKITCSGDRS-----YGYQYQKAPASAPVTVIYANTNRPSDIPS	76
Qy	61	RFSGSLSGSTNLTITGTGQVDEAVYYCGSFD--SSYVGIILGAGTTTLVL	108
Db	77	RFSGSKSGSTATITGTGQADDEAVYYCGSADSSAGIFGAGTTTLVL	125

RESULT 2

A21177  
Ig light chain precursor V-J region - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 21-Jan-2000  
C:Accession: A21177; B22327  
R:Reynaud, C.A.; Dahan, A.; Weill, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 80, 4099-4103, 1983  
A:Title: Complete sequence of a chicken lambda light chain immunoglobulin derived  
A:Reference number: A21177; MUID:83247424; PMID:6408641  
A:Accession: A21177  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-213 <REY>  
A:Cross-references: GB:K00678; NID:q212159; PIDN:AAA48906.1; PID:g212160  
R:Reynaud, C.A.; Anquez, V.; Dahan, A.; Weill, J.C.  
Cell 40, 283-291, 1985  
A:Title: A single rearrangement event generates most of the chicken immunoglobulin  
A:Reference number: A90861; MUID:85099341; PMID:3917859  
A:Accession: B22327  
A:Molecule type: DNA

A:Residues: 98-110 <RE2>

A:Note: J region

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:20-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.4%; Score 430; DB 2; Length 213;

Matches 88; Conservative 6; Mismatches 8; Indels 6; Gaps 3;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWQOKAPASAPVTVIYDNTNRPSNIPS 60

Db 8 ALTPASVSANPGETVKITCSGG---SGS--FGWFOOKSPGAPVTVIYDNRPSNIPS 62

QY 61 RFGSLSGSTNLTITGVQVEDEAVYCGSFDSYVGLGAGTTTLVL 108

Db 63 RFGSKSGSTATLTITGVQAEDEAVYCGSYD-SYVGIFGAGTTTLVL 109

RESULT 3

S49449

Ig lambda chain - duck

C:Species: Anas platyrhynchos (domestic duck)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000

C:Accession: S49449

R:Magor, K.E.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.

submitted to the EMBL Data Library, October 1994

A:Description: cDNA sequence and organization of the immunoglobulin light chain gene of

A:Reference number: S49449

A:Accession: S49449

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-230 <MAG>

A:Cross-references: EMBL:X82069; NID:g558548; PIDN:CAA57568.1; PID:g558549

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-106/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 74.5%; Score 419.5; DB 2; Length 230;

Matches 82; Conservative 6; Mismatches 15; Indels 5; Gaps 1;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWQOKAPASAPVTVIYDNTNRPSNIPS 60

Db 22 ALTPASKSVNPGDTVQITCSGSS-----DYGWFOOKTPGAPVTVIYQNNKRPSPIS 76

QY 61 RFGSLSGSTNLTITGVQVEDEAVYCGSFDSYVGLGAGTTTLVL 108

Db 77 RFGSKSGSTATLTITGVQAEDEAVYCGSYDSSYVGVFGAGTTTLVL 124

RESULT 4

L1CHV

Ig lambda chain precursor V-1 region - chicken

C:Species: Gallus gallus (chicken)

C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 22-Jun-1999

C:Accession: A01992

R:Reynaud, C.A.; Anquez, V.; Dahan, A.; Weill, J.C.

Cell 40, 283-291, 1985

A:Title: A single rearrangement event generates most of the chicken immunoglobulin light

A:Reference number: A90861; MUID:85099341; PMID:3917859

A:Accession: A01992

A:Molecule type: DNA

A:Residues: 1-113 <REY>

A:Cross-references: GB:M12317; NID:g212182; PIDN:AAA50793.1; PID:g212185

A:Note: the sequence was determined from the germline gene

C:Genetics:

A:Introns: 16/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-113/Product: Ig lambda chain V-1 segment #status predicted <LV1>  
F:22-41/Region: framework 1  
F:34-106/Domain: immunoglobulin homology <IMM>  
F:42-49/Region: complementarity-determining 1  
F:50-65/Region: framework 2  
F:66-72/Region: complementarity-determining 2  
F:73-104/Region: framework 3  
F:105-113/Region: complementarity-determining 3  
F:41-104/Disulfide bonds: #status predicted

Query Match 71.7%; Score 403.5; DB 1; Length 113;  
Best Local Similarity 85.1%; Pred. No. 1.4e-28;  
Matches 80; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWQOKAPASAPVTVIYDNTNRPSNIPS 60

Db 22 ALTPSSVSANPGETVKITCSGDRS-----YGYWQOKAPGAPVTVIYDNTNRPSNIPS 76

QY 61 RFGSLSGSTNLTITGVQVEDEAVYCGSFDS 94

Db 77 RFGSKSGSTATLTITGVQADDEAVYCGSADSS 110

RESULT 5

I51216

Ig light chain variable region VL1 - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 19-Mar-1997 #sequence\_revision 07-Nov-1997 #text\_change 21-Jul-2000

C:Accession: I51216

R:Benatar, T.; Ratcliffe, M.J.

Eur. J. Immunol. 23, 2448-2453, 1993

A:Title: Polymorphism of the functional immunoglobulin variable region genes in the

A:Reference number: I51216; MUID:94009199; PMID:8405044

A:Accession: I51216

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-97 <BEN>

A:Cross-references: GB:S65967; NID:g425669; PIDN:AAD13976.1; PID:g4261676

C:Genetics:

A:Gene: Ig VL1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:18-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 68.7%; Score 386.5; DB 2; Length 97;

Matches 77; Conservative 2; Mismatches 10; Indels 5; Gaps 1;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWQOKAPASAPVTVIYDNTNRPSNIPS 60

Db 6 ALTPSSVSANPGTVKITCSGDS-----YGYWQOKAPGAPVTVIYDNTNRPSNIPS 60

QY 61 RFGSLSGSTNLTITGVQVEDEAVYCGSFDS 94

Db 61 RFGSKSGSTATLTITGVQADDEAVYCGSADSS 94

RESULT 6

S05270

Ig lambda chain precursor - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000

C:Accession: S05270; S04601

R:Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A:Reference number: S05270

A:Accession: S05270

A:Molecule type: mRNA

A:Residues: 1-235 <KIS1>

A:Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395

R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains

A:Reference number: S04601; MUID:89296497; PMID:2500644

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associated  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: blocked amino end; heterotetramer

F:15-91/Domain: immunoglobulin homology <IMW>

F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid)

F:22-89/Disulfide bonds: #status predicted

Query Match 55.2%; Score 311; DB 1; Length 111;  
Best Local Similarity 59.3%; Pred. No. 1.7e-20;  
Matches 64; Conservative 12; Mismatches 30; Indels 2; Gaps 2;

OY 2 LTQPSVSNPGETVKITCSGGSYAGSYYGHYQQKAPASAPTVIYDNTNRPSPR 61  
||||| |||| | : |||| | : |||| | : |||| | : |||| | : ||||  
DB 4 LTQPSSVAAPGOEVTCISCGSSNSTGNDFVSWMYO-LPGTAGPLIYDNKRKRGIPDR 62  
  
OY 62 FSGSLGSSTNTLTITGVQVEDEAVVYCGRFSDSS-YVGILGAGTTLVL 108  
||||| |||| | : |||| | : |||| | : |||| | : |||| | : ||||  
DB 63 FSGSKSGTSATLIGTGQTDEADYICGTWDSSLVGMFGGTRIVLV 110

RESULT 9  
LIHUBL  
Ig lambda chain precursor V-I region (BL2) - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 22-Jun-1999  
C:Accession: A01966  
R:Tsujiimoto, Y.; Croce, C.M.  
Nucleic Acids Res. 12, 8407-8414, 1984  
A>Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence  
A:Reference number: A01966; UID:85062823; PMID:6095199  
A:Accession: A01966  
A:Molecule type: mRNA  
A:Residues: 1-130 <FSU>  
A:CROSS-references: GB:X01147; NID:g33335; PIDN:CAA25598.1; PID:g758087  
C:Genetics:  
A:Gene: IGLV6  
A:Cross-references: GDB:l19342; OMIM:147240  
A:Map position: 22q11.2-22q11.2  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associat  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-130/Product: Ig lambda chain V-I region (BL2) #status predicted <MAT>  
F:20-115/Region: V segment  
F:34-110/Domain: immunoglobulin homology <IMM>  
F:116-130/Region: J segment  
F:41-108/Disulfide bonds: #status predicted

Query Match 54.5%; Score 307; DB 1; Length 130;  
Best Local Similarity 58.3%; Pred. No. 4.4e-20;  
Matches 63; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

OY 2 LTQPSVSNPGETVKITCSGGSYAGSYYGHYQQKAPASAPTVIYDNTNRPSPR 61  
||||| |||| | : |||| | : |||| | : |||| | : |||| | : ||||  
DB 23 LTPPPSVSAPOGKVITSCSGSSNGDVSWYQO-VPTGAKPLIIYDNKRKRGIPDR 81  
  
OY 62 FSGSLGSSTNTLTITGVQVEDEAVVYCGRFSDSSVYG-ILGAGTTLVL 108  
||||| |||| | : |||| | : |||| | : |||| | : |||| | : ||||  
DB 82 FSGSKSGTSATLIGTGQTDEADYICGTWNSSLGWVFEGGTRKLVL 129

RESULT 10  
S24321  
Ig lambda chain precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S24321  
R:Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.  
Biochem. J. 285, 149-152, 1992  
A>Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light  
A:Reference number: S24319; UID:92344562; PMID:1379039  
A:Accession: S24321

QY 3 TQPSVSNAPGETVKITCSGGGSYAGSYYYGWYQOKAPASAPVTVIYDNTNRPSNIPSRF 62  
 Db 1 TQPPSVSVSPQOTARITCS-GDALPKQYAY-WYQOK-PGQAPVLVIYKDSRPSGIPERF 57  
 QY 63 SGSLSGSTNTLTITGQVQDEAVYYCGSFDSS--YVGILGAGTTTLVL 108  
 Db 58 SGSSSGTIVTLTISGVQAEADYYCQSDSSGTIV-VFGGGTKTLVL 104

RESULT 13  
 S30526  
 Ig lambda chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S30526  
 R:Mariette, X.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S30520  
 A:Accession: S30526  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <MAR>  
 A:Cross-references: EMBL:Z18332  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:13-89/Domain: immunoglobulin homology <IMM>

Query Match 53.5%; Score 301; DB 2; Length 119;  
 Best Local Similarity 62.6%; Pred. No. 1.3e-19;  
 Matches 67; Conservative 9; Mismatches 27; Indels 4; Gaps 4;

QY 2 LTQPPSVSNAPGETVKITCSGGGSYAGSYYYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 61  
 Db 4 LTQPPSVSVSPQOTARITCS-GDALPKQYAY-WYQOK-PGQAPVLVIYKDSRPSGIPER 60  
 QY 62 FSGSLSGSTNTLTITGQVQDEAVYYCGSFDSSVVGILGAGTTTLVL 108  
 Db 61 FSGSSSGTIVTLTISGVQAEADYYCQSDSS-GPVFGGGTKTLVL 106

RESULT 14  
 S25751  
 Ig lambda chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S25751  
 R:Combrriato, G.; Klobeck, H.G.  
 Eur. J. Immunol. 21, 1513-1522, 1991  
 A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin  
 A:Reference number: S16439; MUID:91257162; PMID:1904362  
 A:Accession: S25751  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-231 <COM>  
 A:Cross-references: EMBL:X57816; NID:g33731; PID:g33732  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:146-214/Domain: immunoglobulin homology <IMM>

Query Match 53.3%; Score 300; DB 2; Length 231;  
 Best Local Similarity 60.7%; Pred. No. 3.3e-19;  
 Matches 65; Conservative 10; Mismatches 28; Indels 4; Gaps 3;

QY 2 LTQPPSVSNAPGETVKITCSGGGSYAGSYYYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 61  
 Db 23 LTQPPSVSVSPGKTASTCS--GDKLGKASWTQKRA-GQSPVLVIYHRSKRPSGIPER 79  
 QY 62 FSGSLSGSTNTLTITGQVQDEAVYYCGSFDSSVVGILGAGTTTLVL 108  
 Db 80 FSGNSNGTATLTISGTQVWDEADYYCQAWDSSIV-VFGGGTKTLVL 125

RESULT 15  
 L4HUHL  
 Ig lambda chain V-IV region (Hil) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-May-1979 #sequence\_revision 31-May-1979 #text\_change 02-Sep-1997  
 C:Accession: A01983  
 R:Rope de Castro, J.A.; Chiu, Y.Y.H.; Poljak, R.J.  
 Biochemistry 17, 1718-1723, 1978  
 A:Title: Amino acid sequence of the variable region of the light (lambda) chain from human  
 A:Reference number: A01983; MUID:78187276; PMID:418804  
 A:Accession: A01983  
 A:Molecule type: protein  
 A:Residues: 1-107 <LOP>  
 A:Note: the sequence of the C region is apparently identical with that of human Sh lambda  
 C:Comment: This chain was isolated from a myeloma protein.  
 C:Genetics:  
 A:Gene: GDB:IGLV6  
 A:Cross-references: GDB:119342; OMIM:147240  
 A:Map position: 22q11.2-22q11.2  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:15-89/Domain: immunoglobulin homology <IMM>  
 F:22-87/Disulfide bonds: #status predicted

Query Match 53.1%; Score 299; DB 1; Length 107;  
 Best Local Similarity 60.7%; Pred. No. 1.8e-19;  
 Matches 65; Conservative 10; Mismatches 28; Indels 4; Gaps 4;

QY 2 LTQPPSVSANPGTIVKTCGGGSGYAGSYGYGQKAPASAPVTIYDNTNRPSNIPSR 61  
 |||| ||| :||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
 Db 4 LTQPPSVSVPGTARITCS-ANALPNQYAY-WYQOK-PGRAPVNVYKDTORPSGIPQR 60  
 |||| ||| :||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
 QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSPDSSYVGLGAGTTLTVL 108  
 |||| ||| :||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
 Db 61 FSSSTSGTTTLTISGVQAEADYCOAWDNS-ASIFGGGTLTVL 106

Search completed: September 3, 2003, 12:16:32  
 Job time : 10.2812 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	403.5	71.7	113	1	LV1D_CHICK	P04210 gallus gall
2	311	55.2	111	1	LV1D_HUMAN	P01702 homo sapien
3	307	54.5	130	1	LV1G_HUMAN	P06316 homo sapien
4	299	53.1	107	1	LV4C_HUMAN	P01717 homo sapien
5	295.5	52.5	112	1	LV6A_HUMAN	P01721 homo sapien
6	295	52.4	106	1	LV4A_HUMAN	P01715 homo sapien
7	292.5	52.0	131	1	LV6E_HUMAN	P06319 homo sapien
8	290	51.5	109	1	LV1I_HUMAN	P06888 homo sapien
9	288	51.2	111	1	LV2B_HUMAN	P01705 homo sapien
10	287	51.0	111	1	LV2C_HUMAN	P01706 homo sapien
11	287	51.0	111	1	LV6D_HUMAN	P06318 homo sapien
12	286	50.8	109	1	LV2E_HUMAN	P01708 homo sapien
13	286	50.8	111	1	LV6C_HUMAN	P06317 homo sapien
14	285	50.6	106	1	LV4E_HUMAN	P06889 homo sapien
15	284	50.4	111	1	LV2A_HUMAN	P01704 homo sapien
16	280	49.7	111	1	LV2D_HUMAN	P01707 homo sapien
17	279.5	49.6	112	1	LV2K_HUMAN	P04209 homo sapien
18	279	49.6	111	1	LV2F_HUMAN	P01709 homo sapien
19	279	49.6	111	1	LV3B_HUMAN	P80748 homo sapien
20	277.5	49.3	110	1	LV2J_HUMAN	P01713 homo sapien
21	277	49.2	108	1	LV3A_HUMAN	P01714 homo sapien
22	277	49.2	109	1	LV1F_HUMAN	P04208 homo sapien
23	272	48.3	106	1	LV4B_HUMAN	P01716 homo sapien
24	272	48.3	111	1	LV2H_HUMAN	P01711 homo sapien
25	268	47.6	111	1	LV1C_HUMAN	P01701 homo sapien
26	267	47.4	106	1	LV4D_HUMAN	P01718 homo sapien
27	267	47.4	111	1	LV2I_HUMAN	P01712 homo sapien
28	265	47.1	111	1	LV2G_HUMAN	P01710 homo sapien
29	262.5	46.6	112	1	LV6B_HUMAN	P01722 homo sapien
30	261	46.4	111	1	LV2L_HUMAN	P80422 homo sapien
31	259.5	46.1	112	1	LV1B_HUMAN	P01700 homo sapien
32	257	45.6	108	1	LV5A_HUMAN	P01719 homo sapien
33	254.5	45.2	112	1	LV1H_HUMAN	P06887 homo sapien

Db 22 ALTPSSVSANPGETVKITCSGDRS-----YGYWQKAPCSADPTLIYDNTNRPSNIPS 76  
QY 61 RFGSLSGSTNTLTITGQVDEAVYCGSFDSS 94  
Db 77 RFGSKSGSATLTITGQADDEAVYCGSADSS 110

## RESULT 2

LV1G\_HUMAN STANDARD; PRT; 111 AA.  
AC P01702;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-I region NIG-64.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN NCBI\_TaxID=9606;  
RP SEQUENCE.  
RX MEDLINE=83186114; PubMed=6404900;  
RA Kamezani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,  
Shimizu A.;  
RT "Comparative studies on the structure of the light chains of human  
immunoglobulins. IV. Assignment of a subgroup.",  
J. Biochem. 93:421-429(1983).  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A01965; LIHUNG.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 105 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 89 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 55.2%; Score 311; DB 1; Length 111;  
Best Local Similarity 59.3%; Pred. No. 3e-23;  
Matches 64; Conservative 12; Mismatches 30; Indels 2; Gaps 2;

QY 2 LTQPSVSANPGETVKITCSGGSYAGSYGYWQKAPASAPVTVIYDNTNRPSNIPSR 61  
Db 4 LTQPPSVSAPGQEVITSCSGSSNIGDYNFVSWYQO-LPGTAPKLLIYDNNKRPSPIDR 62  
QY 62 FSGSLSGSTNTLTITGQVDEAVYCGSFDSSY-VGILGAGTTLTVL 108  
Db 63 FSGSKSGTSATLTITGLTGDEADYCGTWDSLSVGMFGGTRVTVL 110

## RESULT 3

LV1G\_HUMAN STANDARD; PRT; 130 AA.  
AC P06316;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-I region BL2 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN NCBI\_TaxID=9606;  
RP SEQUENCE.  
RX MEDLINE=78187276; PubMed=418804;  
RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;  
RT "Amino acid sequence of the variable region of the light (lambda)  
chain from human myeloma cryoimmunoglobulin IgG HIL";  
Biochemistry 17:1718-1723(1978).  
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY  
IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING  
155-ILE (HIL NUMBERING) INSTEAD OF VAL.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

RP SEQUENCE FROM N.A.  
RX MEDLINE=85062823; PubMed=6095199;  
RA Tsujimoto Y., Croce C.M.;  
RT "Molecular cloning of a human immunoglobulin lambda chain variable  
sequence."; Nucleic Acids Res. 12:8407-8414(1984).  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; X01147; CAA25598.1; -  
DR PIR; A01986; LIHUBL.  
DR HSSP; P01703; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.  
FT DOMAIN 20 115 V SEGMENT.  
FT DOMAIN 116 130 J SEGMENT.  
FT DISULFID 41 108 BY SIMILARITY.  
FT NON\_TER 130 130  
SQ SEQUENCE 130 AA; 13564 MW; FA44BBL7D3A55EBF CRC64;

Query Match 54.5%; Score 307; DB 1; Length 130;  
Best Local Similarity 58.3%; Pred. No. 8.6e-23;  
Matches 63; Conservative 13; Mismatches 30; Indels 2; Gaps 2;

QY 2 LTQPSVSANPGETVKITCSGGSYAGSYGYWQKAPASAPVTVIYDNTNRPSNIPSR 61  
Db 23 LTQPPSVSAPGQEVITSCSGSSNIGDYNFVSWYQO-VGTPAPKLLIYDNNKRPSPIDR 81  
QY 62 FSGSLSGSTNTLTITGQVDEAVYCGSFDSSYVG-ILGAGTTLTVL 108  
Db 82 FSGSKSGTSATLTITGLTGDEADYCGTWDSLSVGMFGGTRVTVL 129

RESULT 4  
LV4C\_HUMAN STANDARD; PRT; 107 AA.  
AC P01717;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig lambda chain V-IV region HIL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN NCBI\_TaxID=9606;  
RP SEQUENCE.  
RX MEDLINE=78187276; PubMed=418804;  
RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;  
RT "Amino acid sequence of the variable region of the light (lambda)  
chain from human myeloma cryoimmunoglobulin IgG HIL";  
Biochemistry 17:1718-1723(1978).  
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY  
IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING  
155-ILE (HIL NUMBERING) INSTEAD OF VAL.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

QY 2 LTQSPSSVSNAPGTVKTKCSG--GGSYAGSYYYGVWQOKAPASAPVTVIYDNTNRPSNIPS 60  
 Db 4 LTQPHSVSESPGKTVTFCTGSGGSIADSFVQ--WYQQR--PGSAPTTVIYDNDNRPSGVPD 61  
 QY 61 RFGSLGSGSTN--TLTITGVQVEDEAVVYCGSFDSSYVGI LGAGTTLTVL 108  
 Db 62 RFGSGIDSANSASLTISGLKTEDEADYYCQSYNSNHVVFGGTKTVTL 111

RESULT 6  
 LV4A\_HUMAN  
 ID LV4A\_HUMAN STANDARD; PRT; 106 AA.  
 AC P01715;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig lambda chain V-IV region Bau.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75059189; PubMed=4435717;  
 RA Baczkó K., Braun D., Hilschmann N.;  
 RT "Pattern of antibody structure, the primary structure of monoclonal  
 RT immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones  
 RT protein Bau.).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:131-154 (1974).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC PIR; A01981; LAHU8U.  
 DR HSSP; P80748; 2LOI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1  
 FT NON\_TER 106 106  
 FT ICD-LIKE.  
 SQ SEQUENCE 106 AA; 11305 MW; 4B6A688E0EC46571 CRC64;

Query Match 52.4%; Score 295; DB 1; Length 106;  
 Best Local Similarity 58.9%; Pred. No. 9.7e-22;  
 Matches 63; Conservative 10; Mismatches 30; Indels 4; Gaps 3

QY 2 LTQSPSSVSNAPGTVKTKCSGSGSYAGSYYYGVWQOKAPASAPVTVIYDNTNRPSNIPS 61  
 Db 3 LTQPPSLSVSPGQASITCS--GDKLGEQVVCWYQQR--FQSPVLVIYHDNRKPSGIPER 59  
 QY 62 FSGSLGSGSTNLTITGVQVEDEAVVYCGSFDSSYVGI LGAGTTLTVL 108  
 Db 60 FSGSNSGTTATLTISGTQAMDEADYYCQAWD--SYTVIFGGTKTVL 105

RESULT 7  
 LV6E\_HUMAN  
 ID LV6E\_HUMAN STANDARD; PRT; 131 AA.  
 AC P06319;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig lambda chain V-VI region EB4 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]

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SEQUENCE FROM N.A.
MEDLINE=85215660; PubMed=3923440;
RA Anderson M.I.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT "Cloning and sequence analysis of an Ig lambda light chain mRNA
expressed in the Burkitt's lymphoma cell line EB4.";
RL Nucleic Acids Res. 13:2931-2941(1985).
DR PIR; A01990; LHUEP.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 131 IG LAMBDA CHAIN V-VI REGION EB4.
FT DOMAIN 20 41 FRAMEWORK-1.
FT DOMAIN 42 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 110 FRAMEWORK-3.
FT DOMAIN 111 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 131 FRAMEWORK-4.
FT DISULFID 41 110 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14147 MW; 02A9179C8C05C2CD CRC64;

Query Match 52.0%; Score 292.5; DB 1; Length 131;
Best Local Similarity 53.2%; Pred. No. 2.1e-21;
Matches 58; Conservative 17; Mismatches 31; Indels 3; Gaps 2;

QY 2 LTQPSVSSANPGETVKITCSGGSYAGSYGYHQKAPASAPVTVIYDNTNRPSNIPSR 61
DB 23 LTQPHSVSPGKTVITISCTGSGSIASNYQVQYQRR-VSAPTIVIEDNQRLGVPDR 81

QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYVILGAGTTLTVL 108
DB 82 FSGSIDSSNSASLTISGLKTEADYQCFDNTNQVFGGKTLTVL 130

RESULT 8
LVII_HUMAN STANDARD; PRT; 109 AA.
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE Ig lambda chain V-I region EPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86000126; PubMed=3929803;
RA Toft K.G., Sletten K., Husby G.;
RT "The amino-acid sequence of the variable region of a carbohydrate-
containing amyloid fibril protein EPS (immunoglobulin light chain,
type lambda).";
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC -1- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
PEPTIDES WERE POSITIONED BY HOMOLOGY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A24656; LHUEP.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid; Glycoprotein.
FT DOMAIN 1 105 IG-LIKE.
FT CARBOHYD 104 104 N-LINKED (GLCNAc. . .).
FT DISULFID 22 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;

Query Match 51.5%; Score 290; DB 1; Length 109;
Best Local Similarity 53.3%; Pred. No. 3e-21;
Matches 57; Conservative 17; Mismatches 31; Indels 2; Gaps 2;

QY 2 LTQPSVSSANPGETVKITCSGGSYAGSYGYHQKAPASAPVTVIYDNTNRPSNIPSR 61
DB 4 LTQPPSLSAAPGQRVSISCSGSSNIGKNYVDWYQQ-LPTAPKLLIFNNKRPSPGIPDR 62

QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYVILGAGTTLTVL 108
DB 63 FSGSKSGTSATLGTITGLTQGTDEAIYCGTWNRR-SVFGGNTNTTV 108

RESULT 9
LV2B_HUMAN STANDARD; PRT; 111 AA.
AC P01705;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region NEI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72233223; PubMed=5043326;
RA Garver F.A., Hilschmann N.;
RT "The primary structure of a monoclonal human lambda-type
immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
RL Eur. J. Biochem. 26:10-32(1972).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01970; L2HUNI.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; Glycoprotein;
KW Pyrolidone carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAc. . .).
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;

Query Match 51.2%; Score 288; DB 1; Length 111;
Best Local Similarity 52.3%; Pred. No. 4.8e-21;
Matches 57; Conservative 19; Mismatches 31; Indels 2; Gaps 2;

QY 1 ALTPQSSVSNPGETVKITCSGGSYAGSY-YYGWYQKAPASAPVTVIYDNTNRPSNIP 59
DB 3 ALTPASVSGSPGQSIITISCTGTSYGVNFVSWYQON-PGKAPKLMIEGNKRPSCVS 61

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QY 60 SRFSGSLGSGTNTLTITGQVQVEDEAVYCGSFSSYVGIIGAGTTLTVL 108
      :||||| ||| : ||||:||||| ||| : : || || |||
Db 62 NRFSGSKGKTASLTISGLQVEADYVCCSYAGNSTRVFGGTRVTVL 110
      :||||| ||| : ||||:||||| ||| : : || || |||

RESULT 10
LV2C_HUMAN
ID LV2C_HUMAN STANDARD; PRT; 111 AA.
AC P01706;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region BOH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75115478; PubMed=804002;
RA Kohler H., Rudofsky S., Kluskens L.;
RT "The primary structure of a human lambda II chain.";
RL J. Immunol. 114:415-421(1975).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE O2+ MARKER.
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01972; L2HUBH.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 106
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90
FT NON_TER 111 111
FT SEQUENCE 111 AA; 11650 MW; 9452030993262388 CRC64;

Query Match 51.0%; Score 287; DB 1; Length 111;
Best Local Similarity 52.3%; Pred. No. 6e-21;
Matches 57; Conservative 17; Mismatches 33; Indels 2; Gaps 2;

QY 1 ALTPQSSVSANPGETVKITCSGGGS-YAGSYYYGYWYQKAPASAPVTVIYDNTNRPSNP 59
      :||||| ||| : ||||:||||| ||| : : || || |||
Db 3 ALTPQPSVSGSPQSVTISCAGTSSDVGGNHVSWYQQH-PGKAPKLIYGVNKRPSGVP 61
      :||||| ||| : ||||:||||| ||| : : || || |||

QY 60 SRFSGSLGSGTNTLTITGQVQVEDEAVYCGSFSSYVGIIGAGTTLTVL 108
      :||||| ||| : ||||:||||| ||| : : || || |||
Db 62 YRFSGSKGNTASLTISGLQAEDEAHYVCCSYAGRTFWFGGTRVTVL 110
      :||||| ||| : ||||:||||| ||| : : || || |||

RESULT 11
LV6D_HUMAN
ID LV6D_HUMAN STANDARD; PRT; 111 AA.
AC P06318;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region WLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86122667; PubMed=4089539;
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RA Dwulet F.E., Strako K., Benson M.D.;
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein (WLT).";
RL Scand. J. Immunol. 22:653-660(1985).
DR PIR; A01989; L6HULT.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 22
FT DOMAIN 23 35
FT DOMAIN 36 50
FT DOMAIN 51 57
FT DOMAIN 58 91
FT DOMAIN 92 101
FT DOMAIN 102 111
FT DISULFID 22 91
FT NON_TER 111 111
FT SEQUENCE 111 AA; 11966 MW; 0C88B2FE37BCE24F CRC64;

Query Match 51.0%; Score 287; DB 1; Length 111;
Best Local Similarity 54.1%; Pred. No. 6e-21;
Matches 59; Conservative 17; Mismatches 29; Indels 4; Gaps 3;

QY 2 LTQPSVSANPGETVKITCSGGGSYAGSYYYGYWYQKAPASAPVTVIYDNTNRPSNP 61
      :||||| ||| : ||||:||||| ||| : : || || |||
Db 4 LTQPLSVSGSPKVTITSGTSSGSGISGYSNVQYQQR-PGSAPTNIYENNRQPSVDPDR 62
      :||||| ||| : ||||:||||| ||| : : || || |||

QY 62 FSGSLGSGTN--TLTITGQVQVEDEAVYCGSFSSYVGIIGAGTTLTVL 108
      :||||| : ||||:||||| ||| : ||||:|||||
Db 63 FSGSIDSSNSASLTISGLKTEADYVCCSYDNNHVVFG-GTRLTVL 110
      :||||| : ||||:||||| ||| : ||||:|||||

RESULT 12
LV2E_HUMAN
ID LV2E_HUMAN STANDARD; PRT; 109 AA.
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80006606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human IgAl immunoglobulin. V. Amino acid sequence of a human IgA lambda light chain (Bur).";
RL J. Biol. Chem. 254:9006-9016(1979).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+ MARKERS.
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01974; L2HUBH.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
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[illegible]

Search completed: September 3, 2003, 12:10:20  
Job time : 6.96875 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:09:30 : Search time 174.656 Seconds  
(without alignments)  
538.192 Million cell updates/sec

Title: US-10-083-424A-26

Perfect score: 563

Sequence: 1 ALTOPSSVSANPGETVKITC.....GSPDSSVVGILGAGTTTLVL'108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

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- 2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep.\*
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- 26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*
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- 31: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	563	100.0	108	26	US-10-083-424a-26

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4	481.5	85.5	257	1	PCT-US02-29003B-57	Sequence 57, Appl
5	463.5	82.3	102	22	US-09-791-537-87221	Sequence 87221, A
6	459.5	81.6	269	23	US-09-830-779-9	Sequence 9, Appl
7	452.5	80.4	102	22	US-09-791-537-129881	Sequence 129881, A
8	450	79.9	105	22	US-09-791-537-86163	Sequence 86163, A
9	449.5	79.8	245	22	US-09-791-537-139118	Sequence 139118, A
10	449	79.8	246	22	US-09-791-537-130347	Sequence 130347, A
11	447	79.4	116	22	US-09-791-537-151022	Sequence 151022, A
12	443	78.7	103	22	US-09-791-537-87234	Sequence 87234, A
13	439	78.0	106	22	US-09-791-537-87166	Sequence 87166, A
14	434	77.1	125	22	US-09-791-537-44409	Sequence 44409, A
15	434	77.1	229	22	US-09-791-537-139316	Sequence 139316, A
16	434	77.1	234	22	US-09-791-537-129944	Sequence 129944, A
17	432	76.7	244	22	US-09-791-537-130346	Sequence 130346, A
18	432	76.7	244	22	US-09-791-537-130378	Sequence 130378, A
19	431.5	76.6	234	22	US-09-791-537-129973	Sequence 129973, A
20	430.5	76.5	119	22	US-09-791-537-81436	Sequence 81436, A
21	430	76.4	108	22	US-09-791-537-86680	Sequence 86680, A
22	430	76.4	108	22	US-09-791-537-86687	Sequence 86687, A
23	430	76.4	213	22	US-09-791-537-44410	Sequence 44410, A
24	429.5	76.3	232	22	US-09-791-537-134932	Sequence 134932, A
25	429	76.2	237	22	US-09-791-537-129974	Sequence 129974, A
26	428	76.0	101	22	US-09-791-537-86714	Sequence 86714, A
27	427.5	75.9	107	22	US-09-791-537-86685	Sequence 86685, A
28	426.5	75.8	258	1	PCT-US02-29003A-55	Sequence 55, Appl
29	426.5	75.8	258	1	PCT-US02-29003B-55	Sequence 55, Appl
30	425.5	75.6	102	22	US-09-791-537-87232	Sequence 87232, A
31	425.5	75.6	253	1	PCT-US02-29003A-51	Sequence 51, Appl
32	425.5	75.6	253	1	PCT-US02-29003A-53	Sequence 53, Appl
33	425.5	75.6	253	1	PCT-US02-29003B-51	Sequence 51, Appl
34	425.5	75.6	253	1	PCT-US02-29003B-53	Sequence 53, Appl
35	424	75.3	103	22	US-09-791-537-87225	Sequence 87225, A
36	423.5	75.2	101	22	US-09-791-537-129942	Sequence 129942, A
37	423.5	75.2	104	22	US-09-791-537-86174	Sequence 86174, A
38	423.5	75.2	253	1	PCT-US02-29003A-1	Sequence 1, Appl
39	423.5	75.2	253	1	PCT-US02-29003A-52	Sequence 52, Appl
40	423.5	75.2	253	1	PCT-US02-29003B-1	Sequence 1, Appl
41	423.5	75.2	253	1	PCT-US02-29003B-52	Sequence 52, Appl
42	423	75.1	101	22	US-09-791-537-86704	Sequence 86704, A
43	423	75.1	101	22	US-09-791-537-86718	Sequence 86718, A
44	423	75.1	101	22	US-09-791-537-87198	Sequence 87198, A
45	423	75.1	108	22	US-09-791-537-86683	Sequence 86683, A

ALIGNMENTS

RESULT 1  
US-10-083-424-26  
; Sequence 26, Application US/10083424  
; GENERAL INFORMATION:  
; APPLICANT: Avicore Biotechnology Institute Inc.  
; TITLE OF INVENTION: Recombinant Scfv Antibodies Specific to Eimeria spp. Respor  
; FILE OF INVENTION: for Coccidiosis  
; FILE REFERENCE: Avicore-USA-1  
; CURRENT APPLICATION NUMBER: US/10/083,424  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: KR 2001-52934  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 26  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: chicken hybridoma cell line 2-1  
US-10-083-424-26

Query Match 100.0%; Score 563; DB 26; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.4e-47;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALTOPSSVSANPGETVKITCSGGSGYAGSYGWTQKAPASAPVTVIYDNTNRPSNIPS 60

Db 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWYQOKAPASAPVTVIYDNTNRPSNIPS 60  
QY 61 RFSGSLSGSTNTLTITGVQVEDEAVYYCGSFDSYVYVILGAGTTTLVL 108  
Db 61 RFSGSLSGSTNTLTITGVQVEDEAVYYCGSFDSYVYVILGAGTTTLVL 108

## RESULT 2

US-10-083-424A-26  
; Sequence 26, Application US/10083424A  
; GENERAL INFORMATION:  
; APPLICANT: Avicore Biotechnology Institute Inc.  
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Elmeria spp. Responsible  
; FILE REFERENCE: for Coccidiosis  
; CURRENT APPLICATION NUMBER: US/10/083,424A  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: KR 2001-52934  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 26  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: chicken hybridoma cell line 2-1  
US-10-083-424A-26

Query Match 100.0%; Score 563; DB 26; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.4e-47;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWYQOKAPASAPVTVIYDNTNRPSNIPS 60  
Db 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWYQOKAPASAPVTVIYDNTNRPSNIPS 60  
QY 61 RFSGSLSGSTNTLTITGVQVEDEAVYYCGSFDSYVYVILGAGTTTLVL 108  
Db 61 RFSGSLSGSTNTLTITGVQVEDEAVYYCGSFDSYVYVILGAGTTTLVL 108

## RESULT 3

PCT-US02-29003A-57  
; Sequence 57, Application PC/TUS0229003A  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten  
; APPLICANT: Forschung e.V.  
; APPLICANT: ZHANG, Mei Yun  
; APPLICANT: SCHILLBERG, Stefan  
; APPLICANT: ZIMMERMANN, Sabine  
; APPLICANT: DI FIORE, Stefano  
; APPLICANT: EMANS, Neil  
; APPLICANT: FISCHER, Rainer  
; TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Methods  
; FILE REFERENCE: of Making and Using  
; CURRENT APPLICATION NUMBER: PCT/US02/29003A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/318,904  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 57  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: scfv N5  
PCT-US02-29003A-57

Query Match 85.5%; Score 481.5; DB 1; Length 257;  
Best Local Similarity 87.2%; Pred. No. 4.6e-39;  
Matches 95; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWYQOKAPASAPVTVIYDNTNRPSNIPS 60  
Db 146 ALTPSSVSANPGETVKITCSGGSYAGSYGYWYQOKSPGAPVTVIYDNTKRPSDIPS 205  
QY 61 RFSGSLSGSTNTLTITGVQVEDEAVYYCGSFDSYVYVILGAGTTTLVL 108  
Db 206 RFSGSKSGSTGTLTITGVQADDEAVYYCGSGDSYSSVIGIFGAGTTTLVL 254

## RESULT 4

PCT-US02-29003B-57  
; Sequence 57, Application PC/TUS0229003B  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten  
; APPLICANT: Forschung e.V.  
; APPLICANT: ZHANG, Mei Yun  
; APPLICANT: SCHILLBERG, Stefan  
; APPLICANT: ZIMMERMANN, Sabine  
; APPLICANT: DI FIORE, Stefano  
; APPLICANT: EMANS, Neil  
; APPLICANT: FISCHER, Rainer  
; TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Meth  
; FILE REFERENCE: of Making and Using  
; CURRENT APPLICATION NUMBER: PCT/US02/29003B  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 60/318,904  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 57  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: scfv N5  
PCT-US02-29003B-57

Query Match 85.5%; Score 481.5; DB 1; Length 257;  
Best Local Similarity 87.2%; Pred. No. 4.6e-39;  
Matches 95; Conservative 4; Mismatches 9; Indels 1; Gaps 1;  
QY 1 ALTPSSVSANPGETVKITCSGGSYAGSYGYWYQOKAPASAPVTVIYDNTNRPSNIPS 60  
Db 146 ALTPSSVSANPGETVKITCSGGSYAGSYGYWYQOKSPGAPVTVIYDNTKRPSDIPS 205  
QY 61 RFSGSLSGSTNTLTITGVQVEDEAVYYCGSFDSYVYVILGAGTTTLVL 108  
Db 206 RFSGSKSGSTGTLTITGVQADDEAVYYCGSGDSYSSVIGIFGAGTTTLVL 254

## RESULT 5

US-09-791-537-87221  
; Sequence 87221, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M  
; FILE REFERENCE: METHODS OF USE THEREOF  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 87221  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-791-537-87221

Query Match 82.3%; Score 463.5; DB 22; Length 102;

Best Local Similarity 86.0%; Pred. No. 9.5e-38;  
Matches 92; Conservative 0; Mismatches 10; Indels 5; Gaps 1;

QY 1 ALTOPSSVSANPGETVKITCSGGSYAGSYYYGWYQKAPASAPVTVIYDNTNRPSNIPS 60

Db 1 ALTOPSSVSANPGETVKITCSGGSS-----YIGWYQKAPGAPVTVIYDNTNRPSNIPS 55

QY 61 RFSGLSGSTNTLTITGVQVEDEAVYYCGSPDSSYVIGLGAGTTTLV 107

Db 56 RFSGSYSTNTLTITGVQAEDEAVYYCASTDSSYAGIFGAGTTTLV 102

## RESULT 6

US-09-830-779-9  
; Sequence 9, Application US/09830779

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; APPLICANT: Chien, Kenneth

; APPLICANT: Dillmann, Wolfgang

; APPLICANT: Minamisawa, Susanne

; APPLICANT: He, Huaping

; APPLICANT: Hoshijima, Masahiko

; APPLICANT: Meyer, Markus

; APPLICANT: Scott, Christopher

; APPLICANT: Wang, Yabin

; APPLICANT: Silverman, Gregg J.

; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT

; FILE REFERENCE: 6627-PA9025

; CURRENT APPLICATION NUMBER: US/09/830,779

; CURRENT FILING DATE: 2001-08-04

; PRIOR APPLICATION NUMBER: 60/106,718

; PRIOR FILING DATE: 1998-11-02

; PRIOR APPLICATION NUMBER: PCT/US99/25692

; PRIOR FILING DATE: 1999-11-02

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 269

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-830-779-9

Query Match 81.6%; Score 459.5; DB 23; Length 269;

Best Local Similarity 81.7%; Pred. No. 7.4e-37;

Matches 89; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 ALTOPSSVSANPGETVKITCSGGSYAGSYYYGWYQKAPASAPVTVIYDNTNRPSNIPS 60

Db 12 ALTHSSVSANPGETVKITCSGGNYAGSYYYGWYQKAPASAPVTVIYDNTNRPSNIPS 71

QY 61 RFSGLSGSTNTLTITGVQVEDEAVYYCGS-FDSSYVIGLGAGTTTLV 108

Db 72 RFSGSTSTLTITGVRAEDEAVYFCGSGTGYVIGFAGGTTTLV 120

## RESULT 7

US-09-791-537-129881

; Sequence 129881, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Blonomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMB

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 129881

; LENGTH: 102

; TYPE: PRT

; ORGANISM: synthetic construct  
US-09-791-537-129881

Query Match 80.4%; Score 452.5; DB 22; Length 102;

Best Local Similarity 85.0%; Pred. No. 1.2e-36;

Matches 91; Conservative 2; Mismatches 9; Indels 5; Gaps 1;

QY 2 LTQPSSVSANPGETVKITCSGGSYAGSYYYGWYQKAPASAPVTVIYDNTNRPSNIPS 61

Db 1 LTQPSSVSANPGETVKITCSGGD-----NYGWYQKAPGAPVTVIYDNTNRPSNIPS 55

QY 62 FSGSLSGSTNTLTITGVQVEDEAVYYCGSPDSSYVIGLGAGTTTLV 108

Db 56 FSGSGSGTGTITGVRAEDEAVYYCGSRDSRGVIGFAGGTTTLV 102

## RESULT 8

US-09-791-537-86163

; Sequence 86163, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Blonomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILI

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 86163

; LENGTH: 105

; TYPE: PRT

; ORGANISM: Gallus gallus

US-09-791-537-86163

Query Match 79.9%; Score 450; DB 22; Length 105;

Best Local Similarity 82.6%; Pred. No. 2.1e-36;

Matches 90; Conservative 4; Mismatches 9; Indels 6; Gaps 2;

QY 1 ALTOPSSVSANPGETVKITCSGGSYAGSYYYGWYQKAPASAPVTVIYDNTNRPSNIPS 60

Db 1 ALTOPASVSANPGETVKITCSGSDS-----SYGWYQKAPGAPVTVIYDNTNRPSNIPS 55

QY 61 RFSGLSGSTNTLTITGVQVEDEAVYYCGSFD-SSYVIGLGAGTTTLV 108

Db 56 RFSGSKSGSTNTLTITGVQAEDEAVYYCGGYDRSTHAGIFGAGTTTLV 104

## RESULT 9

US-09-791-537-139118

; Sequence 139118, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Blonomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILI

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 139118

; LENGTH: 245

; TYPE: PRT

; ORGANISM: synthetic construct

US-09-791-537-139118

Query Match 79.8%; Score 449.5; DB 22; Length 245;

Best Local Similarity 83.2%; Pred. No. 6.5e-36;

Matches 89; Conservative 4; Mismatches 11; Indels 3; Gaps 1;

Qy 2 LTQPSVSANPGETVKITCSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 61  
Db 1 LTQPSVSANPGETVKITCSGGSDSG---YGWYQOKSPGAPVTVIYDNTNRPSNIPSR 57  
Qy 62 FSGSLSGSTNLTITGVQVDEAVYYCGSFDSSVYVGLGAGTTLTVL 108  
Db 58 FSGSGSTNLTITGVQAEDEAVYFCGNRDSYVYGFAGTTLTVL 104

## RESULT 10

US-09-791-537-130347  
; Sequence 130347, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 130347  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-791-537-130347

Query Match 79.8%; Score 449; DB 22; Length 246;  
Best Local Similarity 82.2%; Pred. No. 7.3e-36;  
Matches 88; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

Qy 2 LTQPSVSANPGETVKITCSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 61  
Db 1 LTQPSVSANPGETVKITCSGGSDSG---YGWYQOKSPGAPVTVIYDNTNRPSNIPSR 58  
Qy 62 FSGSLSGSTNLTITGVQVDEAVYYCGSFDSSVYVGLGAGTTLTVL 108  
Db 59 FSGSGSTNLTITGVQAEDEAVYFCGGYGVSTDVGMFGAGTTLTVL 105

## RESULT 11

US-09-791-537-151022  
; Sequence 151022, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 151022  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4)...(4)  
; OTHER INFORMATION: X is an unknown amino acid  
US-09-791-537-151022

Query Match 79.48%; Score 447; DB 22; Length 116;  
Best Local Similarity 83.3%; Pred. No. 4.8e-36;  
Matches 90; Conservative 3; Mismatches 9; Indels 6; Gaps 2;  
Qy 1 LTQPSVSANPGETVKITCSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 60  
Db 14 LTQPSVSANPGETVKITCSGDS-----YGWYQOKSPGAPVTVIYDNTNRPSDIPS 68

Qy 61 RFSGSLSGSTNLTITGVQVDEAVYYCGSFDSSVYVGLGAGTTLTVL 108  
Db 69 RFSGSGSTNLTITGVQAEDEAVYYCGGYDSS-SAIFGAGTTLTVL 115

## RESULT 12

US-09-791-537-87234  
; Sequence 87234, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 87234  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-791-537-87234

Query Match 78.7%; Score 443; DB 22; Length 103;  
Best Local Similarity 80.6%; Pred. No. 1e-35;  
Matches 87; Conservative 7; Mismatches 8; Indels 6; Gaps 2;

Qy 1 ALTOPSSVSANPGETVKITCSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 60  
Db 1 ALTOPSSVSANPGETVKITCSGDS-----YGWYQOKSPGAPVTVIYDNTNRPSNIPSR 55  
Qy 61 RFSGSLSGSTNLTITGVQVDEAVYYCGSFDSSVYVGLGAGTTLTVL 107  
Db 56 RFSGSGSTNLTITGVQAEDEAVYFCGGYEGGTSAGIFGAGTTLTV 103

## RESULT 13

US-09-791-537-87166  
; Sequence 87166, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 87166  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-791-537-87166

Query Match 78.0%; Score 439; DB 22; Length 106;  
Best Local Similarity 78.3%; Pred. No. 2.7e-35;  
Matches 83; Conservative 10; Mismatches 11; Indels 2; Gaps 1;

Qy 1 ALTOPSSVSANPGETVKITCSGGSYAGSYGYGWYQOKAPASAPVTVIYDNTNRPSNIPSR 60  
Db 1 ALTOPASVSANPGETVKITCSGGRYGNGYGYGWYQOKSPGAPVTVIHNDKRPDSIPS 60  
Qy 61 RFSGSLSGSTNLTITGVQVDEAVYYCGSFDSS--YVGLGAGTT 104  
Db 61 RFSGSPGRTTISILLITGVQVDEAVYYCGSFDSSVYVIGIFAGTT 106

## RESULT 14

Search completed: September 3, 2003, 12:49:35  
Job time : 175.756 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	318.5	56.6	108	6	US-10-275-046-67	Sequence 67, Appl
2	308	54.7	109	6	US-10-273-046-75	Sequence 75, Appl
3	305	54.2	109	6	US-10-275-046-89	Sequence 89, Appl
4	305	54.2	110	1	PCT-US03-21304-103	Sequence 103, App
5	304.5	54.1	271	1	US-10-275-589-22	Sequence 22, Appl
6	304	54.0	109	6	US-10-273-046-79	Sequence 79, Appl
7	304	54.0	109	6	US-10-275-046-91	Sequence 91, Appl
8	301	53.5	109	6	US-10-275-046-71	Sequence 71, Appl
9	301	53.5	109	6	US-10-275-046-85	Sequence 85, Appl
10	301	53.5	109	6	US-10-275-046-95	Sequence 95, Appl
11	300.5	53.4	111	7	US-60-485-404-70	Sequence 70, Appl
12	300.5	53.4	232	6	US-10-291-265-755	Sequence 755, App
13	300	53.3	239	6	US-10-275-046-77	Sequence 77, Appl
14	300	53.3	111	6	US-10-275-046-87	Sequence 87, Appl
15	300	53.3	216	6	US-10-273-573-6265	Sequence 6265, Ap
16	300	53.3	231	6	US-10-291-265-283	Sequence 283, App
17	299.5	53.2	232	6	US-10-291-265-343	Sequence 343, App
18	299	53.1	109	6	US-10-275-046-59	Sequence 59, Appl
19	299	53.1	109	6	US-10-275-046-73	Sequence 73, Appl
20	297	52.8	109	6	US-10-273-046-81	Sequence 81, Appl
21	297	52.8	109	6	US-10-275-046-97	Sequence 97, Appl
22	297	52.8	245	1	PCT-US03-25457-47	Sequence 47, Appl
23	295	52.4	147	6	US-10-286-897-2652	Sequence 2652, Ap
24	295	52.4	147	6	US-10-258-898A-2652	Sequence 2652, Ap
25	295	52.4	147	1	PCT-US03-25457-45	Sequence 45, Appl
26	294.5	52.3	245	1	PCT-US03-15937-57	Sequence 57, Appl

```

RESULT 4
PCT-US03-21304-103
; Sequence 103, Application PC/TUS0321304
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; FILE REFERENCE: 053693-5050WO
; CURRENT APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,356
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens

```

```

RESULT 6.
US-10-275-046-79
; Sequence 79, Application US/10275046
; GENERAL INFORMATION:
; APPLICANT: Nagy et al.
; TITLE OF INVENTION: IMMUNOMODULATORY
; FILE REFERENCE: GPCG-P01-260
; CURRENT APPLICATION NUMBER: US/10/275
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 00110063.5
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MS-GPC14 VL
US-10-275-046-79

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Query Match 54.0%; Score 304; DB 6; Length 109;



QY 2 LTQPSSVSANPGETVKITCSGGGSYAGSYYYGWYQQKAPASAPVTVIYDNTNRPSNIPSR 61

**Qy** 62 FSGSLGSGTNTLTITGVQVEDEAVYYCGSFDSSYYCILGAGTTTLTVL 108  
|||||:::|||||:|||||:|||||:|||||:

**Db** 63 FSGKSGTSALAITGLOSEADYYCOSYDYDHY-VFGSGTKLTVL 108

RESULT 11  
US-60-485-404-70  
; Sequence 70, Application US/60485404  
; GENERAL INFORMATION:  
; APPLICANT: Prior, Christopher P.  
; APPLICANT: Turner, Andrew J.  
; APPLICANT: Sadegh, Homayoun  
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries  
; FILE REFERENCE: 054710-5007-PR  
; CURRENT APPLICATION NUMBER: US/60/485,404  
; CURRENT FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: US 10/231,494  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 60/406,997  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 10/384,060  
; PRIOR FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: US 60/460,829  
; PRIOR FILING DATE: 2003-04-08  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: VL region of anti-TNF-alpha/ScFv antibody  
US-60-485-404-70

Query Match 53.4%; Score 300.5; DB 7; Length 111;  
Best Local Similarity 57.8%; Pred. No. 1.4e-16;  
Matches 63; Conservative 14; Mismatches 29; Indels 3; Gaps 3;  
QY 2 LTQPSSVSANPGTGVKTCGGGSGYAGS-YYGYGQOKAPASAPVTIVYDNTNRPSNIPS 60  
DB 4 LTQPSSVSANPGTGVKTCGGGSGYAGS-YYGYGQOKAPASAPVTIVYDNTNRPSNIPS 60  
QY 61 RFGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYG-ILGAGTTTLTVL 108  
DB 63 RFGSKSGTSASLAITGLQAEDEADYCYQSYDYG-IYVFGGKTLTVL 111

RESULT 12  
US-10-291-265-755  
; Sequence 755, Application US/10291265  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang et al.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; CURRENT APPLICATION NUMBER: US/10/291,265  
; CURRENT FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 755  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-291-265-755

Query Match 53.4%; Score 300.5; DB 6; Length 232;  
Best Local Similarity 58.9%; Pred. No. 2.7e-16;  
Matches 63; Conservative 10; Mismatches 31; Indels 3; Gaps 2;

QY 2 LTQPSSVSANPGTGVKTCGGGSGYAGS-YYGYGQOKAPASAPVTIVYDNTNRPSNIPS 61  
DB 23 LTQPSSVSANPGTGVKTCGGGSGYAGS-YYGYGQOKAPASAPVTIVYDNTNRPSNIPS 61  
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYG-ILGAGTTTLTVL 108  
DB 80 FSGNSGNTATLTISGTQAMDEADYCYQSYDYG-IYVFGGKTLTVL 126

RESULT 13  
US-10-275-046-77  
; Sequence 77, Application US/10275046  
; GENERAL INFORMATION:  
; APPLICANT: Nagy et al.  
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPT  
; FILE REFERENCE: GPCG-P01-260  
; CURRENT APPLICATION NUMBER: US/10/275,046  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: 00110063.5  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 77  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MS-GPC11 VL  
US-10-275-046-77

Query Match 53.3%; Score 300; DB 6; Length 109;  
Best Local Similarity 57.0%; Pred. No. 1.5e-16;  
Matches 61; Conservative 12; Mismatches 32; Indels 2; Gaps 2;  
QY 2 LTQPSSVSANPGTGVKTCGGGSGYAGS-YYGYGQOKAPASAPVTIVYDNTNRPSNIPS 61  
DB 4 LTQPSSVSANPGTGVKTCGGGSGYAGS-YYGYGQOKAPASAPVTIVYDNTNRPSNIPS 62  
QY 62 FSGSLSGSTNTLTITGVQVEDEAVYCGSFSSVYG-ILGAGTTTLTVL 108  
DB 63 FSGSKSGTSASLAITGLQSEDEADYCYQSYDYG-IYVFGGKTLTVL 108

RESULT 14  
US-10-275-046-87  
; Sequence 87, Application US/10275046  
; GENERAL INFORMATION:  
; APPLICANT: Nagy et al.  
; TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPT  
; FILE REFERENCE: GPCG-P01-260  
; CURRENT APPLICATION NUMBER: US/10/275,046  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: 00110063.5  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 87  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MS-GPC-8-10  
US-10-275-046-87

Query Match 53.3%; Score 300; DB 6; Length 111;  
Best Local Similarity 56.5%; Pred. No. 1.6e-16;  
Matches 61; Conservative 12; Mismatches 33; Indels 2; Gaps 2;  
QY 2 LTQPSSVSANPGTGVKTCGGGSGYAGS-YYGYGQOKAPASAPVTIVYDNTNRPSNIPS 61  
DB 4 LTQPSSVSANPGTGVKTCGGGSGYAGS-YYGYGQOKAPASAPVTIVYDNTNRPSNIPS 62

OY 62 FSGSLGGSTNTLTITGQVDEAVYYCGSFDSSVY-ILGAGTTLTVL 108  
|||||:::| ||||| ||||| |||||:::| |||||  
Db 63 FSGSKGTSASLAITGLQSEDEADYYCQSYDYDLIRHVFGGTKTLTVL 110

RESULT 15  
US-10-273-573-6265  
; Sequence 6265, Application US/10273573  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-066  
; CURRENT APPLICATION NUMBER: US/10/273,573  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 09/522,929  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/770,160  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 10994  
; SOFTWARE: Custom  
; SEQ ID NO 6265  
; LENGTH: 216  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (163)..(186)  
; OTHER INFORMATION: Immunoglobulins and major histocompatibility complex proteins  
; OTHER INFORMATION: domain identified by eMatrix, accession number BL00290A, p-value-  
; OTHER INFORMATION: 1.529e-14, raw score of 20.89  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (43)..(213)  
; OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name ig,  
; OTHER INFORMATION: E-value=3.4e-15, Pfam score of 54.0  
US-10-273-573-6265

Query Match 53.3%; Score 300; DB 6; Length 216;  
Best Local Similarity 54.6%; Pred. No. 2.8e-16;  
Matches 59; Conservative 17; Mismatches 30; Indels 2; Gaps 2;  
OY 2 LTQPSVSANPGTVMKTCGGGSGYAGSYGYGQKAPASAPVTVIYDNTNRPSNIPSR 61  
||||| |||||:::| ||||| ||||| |||||:::| |||||  
Db 32 LTQPPSVSAAPGQQITISGSRNLNVGNFYVSWYQQ-LPGTAPKILIYDNDKRPSPDAR 90  
OY 62 FSGSLGGSTNTLTITGQVDEAVYYCGSFDSSVYV-ILGAGTTLTVL 108  
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Db 91 FSGSKGTSATLAITGLQTGDEANYCYGAWDTSLDNNVFGGTEVTVL 138

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GenCore version 5.1.6  
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OM protein - protein search, using sw model.

Run on: September 3, 2003, 12:00:29 ; Search time 35.6615 Seconds  
(without alignments)  
547.464 Million cell updates/sec

Title: US-10-083-424A-18  
Perfect score: 663  
Sequence: 1 AVTLDESGLQTPGALS.....AGCGDIDANGHTEIVSS 123

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	79.9	146	19	AAW60170
2	507	76.5	129	22	AAW60170
3	496.5	74.9	141	19	AAW60172
4	494.5	74.6	147	19	AAW60173
5	487	73.5	269	21	AAW71010
6	478.5	72.2	145	19	AAW60171
7	403.5	60.9	177	24	ABJ36939
8	401	60.5	138	21	AAJ32406
9	400.5	60.4	253	24	ABJ19830
					Chicken Mab heavy
					Chicken protein #1
					Heavy chain variab
					Heavy chain variab
					Chicken phospholam
					Heavy chain variab
					Anti-CD40 monoclon
					Mouse anti-verotox
					Human VEGF-2 relat

10	399	60.2	384	22	AAW24101	Human EST encoded
11	395.5	59.7	95	23	ABG60414	Selective targetin
12	394	59.4	221	24	ABR01534	Human anti-TIMP-1
13	393.5	59.4	222	24	ABR01515	Human anti-TIMP-1
14	393	59.3	127	22	AAG33584	Human anti-Rh(D) c
15	392.5	59.2	224	24	ABR01513	Human anti-TIMP-1
16	392.5	59.2	239	23	ABP46012	Human BLYS binding
17	392.5	59.2	240	22	ABA46051	Human TF anti-idio
18	390.5	58.9	122	20	AAV43253	VH domain CDR of a
19	390.5	58.9	249	23	ABP45094	Human BLYS binding
20	390.5	58.9	253	20	AAW90225	Anti-B7.1 monospec
21	390.5	58.9	258	20	AAW90221	Anti-B7.1 monospec
22	390.5	58.9	268	20	AAW90228	Anti-B7.1/anti-B7.
23	390.5	58.9	273	20	AAW90224	Anti-B7.1/anti-B7.
24	390.5	58.9	556	20	AAW90218	Bispecific tetra
25	390.5	58.9	580	20	AAW90217	Bispecific tetra
26	390	58.8	117	22	AAE12061	Human anti-tissue
27	390	58.8	123	18	AAW15534	Anti-TGF beta-1 sc
28	389.5	58.7	239	23	ABP46011	Human BLYS binding
29	389.5	58.7	247	23	ABP44985	Human BLYS binding
30	388.5	58.6	120	23	AAO18449	Anti-GD2 antibody
31	388.5	58.6	249	23	ABP44881	Human BLYS binding
32	388.5	58.6	249	23	ABP44885	Human BLYS binding
33	388	58.5	125	23	ABG77142	Anti-TGF-IR antio
34	387.5	58.4	140	18	AAW13524	Anti-melanoma anti
35	387.5	58.4	254	23	ABP45690	Human BLYS binding
36	387	58.4	248	23	ABP44902	Human BLYS binding
37	387	58.4	470	23	ABG77158	Germline protein s
38	386.5	58.3	118	23	AAO18441	Anti-GD2 antibody
39	386.5	58.3	131	18	AAW13520	Anti-melanoma anti
40	386.5	58.3	136	24	ABP55473	Synthetic 3-23 VH
41	386.5	58.3	240	22	AAW60007	Human MUC-1 scFv c
42	386.5	58.3	367	24	ABP55467	MALIA3 protein seq
43	386	58.2	115	21	ABP39519	Anti-IL12 antibody
44	385.5	58.1	118	23	AAU83803	MS-GPC-6 heavy cha
45	385.5	58.1	118	23	ABB57561	HLA-DR-specific pr

ALIGNMENTS

RESULT 1	
AAW60170	
ID	AAW60170 standard; Protein; 146 AA.
XX	
AC	AAW60170;
XX	
DT	23-SEP-1998 (first entry)
XX	
DE	Chicken Mab heavy chain variable domain sequence.
XX	
KW	Chicken; monoclonal antibody; MAB; immortalisation; immunisation;
KW	cystic fibrosis transmembrane conductance regulator; cystic fibrosis;
KW	B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;
KW	transforming growth factor beta; CFTR; TGF beta.
OS	Gallus sp.
XX	
PN	WO9822510-A2.
XX	
PD	28-MAY-1998.
XX	
PF	18-NOV-1997; 97WO-US21077.
XX	
PR	18-NOV-1996; 96US-0751359.
XX	
PA	(ARCH-) ARCH DEV CORP.
PA	(UABR-) UAB RES FOUND.
XX	
PI	Accavitti MAV, Michael NM, Thompson CB;
XX	
DR	WPI; 1998-312421/27.
XX	



XX Accavitti MAV, Michael NM, Thompson CB;  
 XX WPI; 1998-312421/27.  
 XX  
 XX Production of new monoclonal antibodies - by immunising chickens and  
 PT immortalising B cells, used for, e.g. diagnosis and passive  
 PT treatment of disease  
 XX  
 XX Example 2; Page 61; 97pp; English.  
 XX  
 XX This represents the amino acid sequence of the heavy chain variable  
 CC domain of anti-CFTR 15-16. The invention provides a method for producing  
 CC chicken monoclonal antibodies (MAB) against a variety of antigens. The  
 CC method comprises immunising a chicken with an antigen and isolating and  
 CC immortalising B cells. From a selected antibody-producing B cell,  
 CC nucleic acid containing antigen-binding exons of the light and heavy  
 CC chain genes is prepared. The heavy and light chain nucleic acid are  
 CC cloned separately in vectors that encode the constant and leader  
 CC regions of the heavy and light chains. The vectors are transferred to  
 CC host cells which are cultured and the MAB is isolated. Such antibodies  
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),  
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-  
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and  
 CC carbohydrates. The MAB can be raised against antigenic determinants that  
 CC do not normally induce a response in mammals. The structure of the  
 CC chicken immunoglobulin (Ig) gene is such that even after diversification  
 CC by repeated gene conversions and maturation, the genomic DNA of the  
 CC expressed locus will always have the same L-V (leader-variable) intron  
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the  
 CC antigen-binding domain of rearranged chicken genes are known with  
 CC certainty, allowing specific amplification with a single set of primers.  
 CC The method is particularly used to produce MAB against mammalian antigens  
 CC with highly conserved epitopes. The MABs are used for separation,  
 CC detection, quantification or removal of antigens, particularly for  
 CC diagnosis, including in vivo imaging. They are useful as  
 CC immunohistochemical reagents, and for passive treatment of diseases,  
 CC such as cystic fibrosis.  
 XX  
 SQ Sequence 141 AA;  
 Query Match 74.98; Score 496.5; DB 19; Length 141;  
 Best Local Similarity 81.39; Pred. No. 4.8e-36;  
 Matches 100; Conservative 4; Mismatches 18; Indels 1; Gaps 1;  
 QY 1 AVTLDESGGGLQTPGGGLSLVCKASGFTFSSHGMMWVROTTPGKLEWVAGISNTGTYY 60  
 DB 20 AVTLDESGGGLQTPGGGLSLVCKASGFTFSSHGMMWVROTTPGKLEWVAGISNTGTYY 79  
 QY 61 APYVGRATISRDNGQSTVRLQLNLNLAEDTGTYYCAKGGAYCAGCGGDDAWGHGTEVI 120  
 DB 80 GSAVGRATISRDNGQSTVRLQLNLNLAEDTGTYYCAKGGAYCAGCGGDDAWGHGTEVI 138  
 QY 121 VSS 123  
 DB 139 VSS 141  
 QY  
 DB  
 XX  
 XX AAW60173 standard; Protein; 147 AA.  
 XX  
 XX AAW60173;  
 XX  
 XX 23-SEP-1998 (first entry)  
 XX  
 XX Heavy chain variable domain sequence of antibody 8 of unknown specificity.  
 XX  
 KW Chicken; monoclonal antibody; MAB; immortalisation; immunisation;  
 KW cystic fibrosis transmembrane conductance regulator; cystic fibrosis;  
 KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;  
 KW transforming growth factor beta; CFTR; TGF beta.  
 XX

OS Gallus sp.  
 XX  
 XX WO9822510-A2.  
 XX  
 XX 28-MAY-1998.  
 XX  
 XX 18-NOV-1997; 97WO-US21077.  
 XX  
 XX 18-NOV-1996; 96US-0751359.  
 XX  
 XX (ARCH-) ARCH DEV CORP.  
 XX (UABR-) UAB RES FOUND.  
 XX  
 XX Accavitti MAV, Michael NM, Thompson CB;  
 XX WPI; 1998-312421/27.  
 XX  
 XX Production of new monoclonal antibodies - by immunising chickens and  
 PT immortalising B cells, used for, e.g. diagnosis and passive  
 PT treatment of disease  
 XX  
 XX Example 2; Page 61; 97pp; English.  
 XX  
 XX This represents the heavy chain variable domain of an antibody of unknown  
 CC specificity used as a control. The invention provides a method for  
 CC producing chicken monoclonal antibodies (MAB) against a variety of  
 CC antigens. The method comprises immunising a chicken with an antigen and  
 CC isolating and immortalising B cells. From a selected antibody-producing  
 CC B cell, nucleic acid containing antigen-binding exons of the light and  
 CC heavy chain genes is prepared. The heavy and light chain nucleic acid are  
 CC cloned separately in vectors that encode the constant and leader  
 CC regions of the heavy and light chains. The vectors are transferred to  
 CC host cells which are cultured and the MAB is isolated. Such antibodies  
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),  
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-  
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospho)lipids and  
 CC carbohydrates. The MAB can be raised against antigenic determinants that  
 CC do not normally induce a response in mammals. The structure of the  
 CC chicken immunoglobulin (Ig) gene is such that even after diversification  
 CC by repeated gene conversions and maturation, the genomic DNA of the  
 CC expressed locus will always have the same L-V (leader-variable) intron  
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the  
 CC antigen-binding domain of rearranged chicken genes are known with  
 CC certainty, allowing specific amplification with a single set of primers.  
 CC The method is particularly used to produce MAB against mammalian antigens  
 CC with highly conserved epitopes. The MABs are used for separation,  
 CC detection, quantification or removal of antigens, particularly for  
 CC diagnosis, including in vivo imaging. They are useful as  
 CC immunohistochemical reagents, and for passive treatment of diseases,  
 CC such as cystic fibrosis.  
 XX  
 SQ Sequence 147 AA;  
 Query Match 74.6%; Score 494.5; DB 19; Length 147;  
 Best Local Similarity 78.9%; Pred. No. 7.5e-36;  
 Matches 101; Conservative 5; Mismatches 17; Indels 5; Gaps 2;  
 QY 1 AVTLDESGGGLQTPGGGLSLVCKASGFTFSSHGMMWVROTTPGKLEWVAGISNTGTYY 60  
 DB 20 AVTLDESGGGLQTPGGGLSLVCKASGFTFSSHGMMWVROTTPGKLEWVAGISNTGTYY 79  
 QY 61 APYVGRATISRDNGQSTVRLQLNLNLAEDTGTYYCAKGGAYCAGCGGDDAWGH 115  
 DB 80 APYVGRATISRDNGQSTVRLQLNLNLAEDTGTYYCAKGGAYCAGCGGDDAWGH 139  
 QY 116 GTEVIVSS 123  
 DB 140 GTEVIVSS 147  
 XX  
 XX  
 XX RESULT 5  
 XX AAY71010  
 XX ID AAY71010 standard; Protein; 269 AA.

XX AC AAY71010;  
 XX DT 29-AUG-2000 (first entry)  
 XX DE Chicken phospholamban (PLB) antibody, contractilin.  
 XX KW Phospholamban; PLB; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;  
 KW cardiomyocyte; transport peptide; penetratin; cargo peptide; chicken;  
 KW contractilin; cardiac contractility; inhibitor; cardiac disease;  
 KW cardiant; treatment; heart failure; myocardial dysfunction.  
 XX OS Gallus domesticus.  
 XX PN WO200025804-A2.  
 XX PD 11-MAY-2000.  
 XX PF 02-NOV-1999; 99WO-US25692.  
 XX PR 02-NOV-1998; 98US-0106718.  
 XX PR 27-JUL-1999; 99US-0145883.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Chien K, Dillman W, Minamisawa S, He H, Hoshijima M, Meyer M;  
 XX PI Scott C, Wang Y, Silverman GJ;  
 XX DR WPI: 2000-365393/31.  
 XX PT Treating cardiac diseases, e.g. heart failure or myocardial dysfunction  
 PT comprises enhancing cardiac contractility by inhibiting interaction  
 PT between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine  
 PT triphosphatase  
 XX PS Disclosure; Page 50-51; 56pp; English.  
 XX CC The patent discloses a method for the treatment of heart failure, using  
 CC small peptide complexes and recombinant proteins, that induces  
 CC phospholamban (PLB) deficiency and inhibits the interaction between PLB  
 CC and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes.  
 CC The peptide complex comprises of transport peptide like penetratin and  
 CC cargo peptide selected from mutant PLB, native PLB or antibody against  
 CC PLB protein (contractilin). Penetratin-PLB peptide functions as a  
 CC dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac  
 CC contractility and reduces blood pressure. This method is useful for the  
 CC treatment of cardiac disease e.g. heart failure and myocardial  
 CC dysfunction. The present sequence is that of contractilin protein, a  
 CC chicken antibody peptide with hyperactive regions. This is used to raise  
 CC polyclonal PLB antibody, by immunising a chicken repeatedly with the  
 CC human PLB peptide from the cytoplasmic domain (residues 3-19).  
 XX SQ Sequence 269 AA;  
 Query Match 73.5%; Score 487; DB 21; Length 269;  
 Best Local Similarity 77.0%; Pred. No. 6.6e-35;  
 Matches 97; Conservative 6; Mismatches 17; Indels 6; Gaps 3;  
 QY 2 VTLDESGGLQTPGGALSLVCKASGFTSSHGMMVVRQTPGKLEWVAGISNTGYTYA 61  
 DB 129 VTLDESGGLQTPGGALSLVCKASGFTSSHGMMVVRQTPGKLEWVAGIDBGGSTLYG 188  
 QY 62 PAVKGRATISRDNGQSTVRLQNLNLRADDTGYTCAGKAGYACAG--CGGD-IDAWGHGT 117  
 DB 189 AAVKGRATILRDNGQSTVRLQDLNLRPEDTATYFCVK--TKCGNGWCGADRIDAWGHGT 246  
 QY 118 EVIVSS 123  
 DB 247 EVIVSS 252

RESULT 6  
 AAW60171

ID AAW60171 standard; Protein; 145 AA.  
 XX AC AAW60171;  
 XX DT 23-SEP-1998 (first entry)  
 XX DE Heavy chain variable domain sequence of anti-CFTR 4-9.  
 XX KW Chicken; monoclonal antibody; MAB; immortalisation; immunisation;  
 KW cystic fibrosis transmembrane conductance regulator; cystic fibrosis;  
 KW B cell; passive treatment; cystic fibrosis; cyclin-dependent kinase;  
 KW transforming growth factor beta; CFTR; TGF beta.  
 XX OS Gallus sp.  
 XX PN WO9822510-A2.  
 XX PD 28-MAY-1998.  
 XX PF 18-NOV-1997; 97WO-US21077.  
 XX PR 18-NOV-1996; 96US-0751359.  
 XX PA (ARCH-) ARCH DEV CORP.  
 XX PI (UABR-) UAB RES FOUND.  
 XX PI Accavitti MAV, Michael NM, Thompson CB;  
 XX DR WPI: 1998-312421/27.  
 XX PT Production of new monoclonal antibodies - by immunising chickens and  
 PT immortalising B cells, used for, e.g. diagnosis and passive  
 PT treatment of disease  
 XX PS Example 2; Page 61; 97pp; English.  
 XX CC This represents the amino acid sequence of the heavy chain variable  
 CC domain of anti-CFTR 4-9. The invention provides a method for producing  
 CC chicken monoclonal antibodies (MAB) against a variety of antigens. The  
 CC method comprises immunising a chicken with an antigen and isolating and  
 CC immortalising B cells. From a selected antibody-producing B cell,  
 CC nucleic acid containing antigen-binding exons of the light and heavy  
 CC chain genes is prepared. The heavy and light chain nucleic acid are  
 CC cloned separately in vectors that encode the constant and leader  
 CC regions of the heavy and light chains. The vectors are transferred to  
 CC host cells which are cultured and the MAB is isolated. Such antibodies  
 CC can bind to CFTR (cystic fibrosis transmembrane conductance regulator),  
 CC TGF beta (transforming growth factor beta), transcription factors, DNA-  
 CC or RNA-binding molecules, cyclin-dependent kinases, (phospholipids and  
 CC carbohydrates). The MAB can be raised against antigenic determinants that  
 CC do not normally induce a response in mammals. The structure of the  
 CC chicken immunoglobulin (Ig) gene is such that even after diversification  
 CC by repeated gene conversions and maturation, the genomic DNA of the  
 CC expressed locus will always have the same L-V (leader-variable) intron  
 CC and J (junction)-3' flanking sequences. Thus the sequences flanking the  
 CC antigen-binding domain of rearranged chicken genes are known with  
 CC certainty, allowing specific amplification with a single set of primers.  
 CC The method is particularly used to produce MAB against mammalian antigens  
 CC with highly conserved epitopes. The MABs are used for separation,  
 CC detection, quantification or removal of antigens, particularly for  
 CC diagnosis, including in vivo imaging. They are useful as  
 CC immunohistochemical reagents, and for passive treatment of diseases,  
 CC such as cystic fibrosis.  
 XX SQ Sequence 145 AA;

Query Match 72.2%; Score 478.5; DB 19; Length 145;  
 Best Local Similarity 77.2%; Pred. No. 1.9e-34;  
 Matches 98; Conservative 6; Mismatches 18; Indels 5; Gaps 2;

QY 1 AVTLDESGGLQTPGGALSLVCKASGFTSSHGMMVVRQTPGKLEWVAGISNTGYTYA 60  
 DB 20 AVTLDESGGLQTPRGALSLVCKASGFTT-SYLMHVVRAQPGKLEWVGIRSDGSKTGY 78



frameworks, provided that at least 1 position selected from Asp, H25, H30, H49 and H98 is occupied by the amino acid at the equivalent position of the MuVtm1-1 antibody heavy or light chain variable region (see AAY32406-07) have an affinity framework. Such humanized antibodies (see AAY32406-07) have an affinity framework.

CC for vnt2 that is 3-, 5 or 10-times that of MuVtm1-1. They are used for  
 CC treating a patient suffering from, or at risk of, the toxic effects  
 CC from vnt2 (claimed), especially for treating verotoxin producing  
 CC Escherichia coli (VTEC) infection, and haemolytic uraemic syndrome  
 CC (HUS).  
 XX  
 SQ Sequence 138 AA;  
 Query Match 60.5%; Score 401; DB 21; Length 138;  
 Best Local Similarity 64.8%; Pred. No. 1.1e-27;  
 Matches 79; Conservative 12; Mismatches 27; Indels 4; Gaps 1;  
 QY 2 VTDESGLGQTGGALSLVCKASGFTSSHGMMVVRQTPGKGLWVAGISNTGTYTYA 61  
 Db 21 VQLVESGGGLVQPGGSLRLCAASGFTSSYGMVVRQAPGKGLWVATISGGSYTYP 80  
 QY 62 PAVKGRATISRDNGQSTVRLQLNNLRADDTGYTCAGKAYCAGCGGIDDAWGHGTEVIV 121  
 Db 81 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYICARRG-----DAWGNLDYWGOGTLTV 136  
 QY 122 SS 123  
 Db 137 SS 138  
 RESULT 9  
 ABJ19830  
 ID ABJ19830 standard; Protein; 253 AA.  
 AC ABJ19830;  
 XX  
 DT 10-APR-2003 (first entry)  
 DE Human VEGF-2 related protein SEQ ID NO 76.  
 KW Cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic;  
 KW antithritic; antidiabetic; ophthalmological; antiallergic;  
 KW immunosuppressive; dermatological; antipsoriatic; vulnerary; antibody;  
 KW CDR region; VH domain; VL domain; immunospecific; VEGF-2; cancer;  
 KW proliferative disorder; cardiovascular disorder; arrhythmia;  
 KW cerebrovascular disorder; cerebral anoxia; inflammatory disease;  
 KW infectious disease; autoimmune disease; rheumatoid arthritis;  
 KW Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis;  
 KW angiogenesis; wound healing; vascular tissue repair; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283704-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 12-APR-2002; 2002WO-US11474.  
 XX  
 PR 13-APR-2001; 2001US-283385P.  
 PR 24-JAN-2002; 2002US-350366P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Albert VR, Ruben SM, Wager RE;  
 XX  
 DR WPI; 2003-092991/08.  
 XX  
 DR New isolated polynucleotide encoding an antibody which inhibits a  
 PT VEGF-2 polypeptide, useful for diagnosing, treating or preventing  
 PT diseases associated with aberrant VEGF-2 expression or function, e.g.  
 PT cancer or inflammation  
 XX  
 PS Disclosure; Page 386-387; 425pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide encoding a first  
 CC antibody at least 95-100% identical to a second antibody comprising an  
 CC amino acid sequence selected from at least one, two or three CDR  
 CC region(s) of a VH or VL domain where the first antibody

CC immunospecifically inhibits a VEGF-2 polypeptide. The isolated  
 CC polynucleotide is useful in diagnosing, treating, preventing, prognosing,  
 CC ameliorating or monitoring diseases associated with aberrant VEGF-2 or  
 CC VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function,  
 CC such as cancer and other proliferative disorders, cardiovascular  
 CC disorders (arrhythmias), cerebrovascular disorders (e.g. cerebral  
 CC anoxia), inflammatory diseases, infectious diseases, autoimmune diseases  
 CC (e.g. rheumatoid arthritis, systemic lupus erythematosus, allergies),  
 CC diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and  
 CC antibodies may also be used to stimulate angiogenesis, wound healing, and  
 CC promoting vascular tissue repair. The polynucleotide and polypeptide may  
 CC also be used for in vitro purposes related to scientific research,  
 CC synthesis of DNA and manufacture of DNA vectors, and for the production  
 CC of diagnostics and therapeutics to treat human diseases. This sequence  
 CC represents a human VEGF-2 related protein of the invention.  
 XX  
 SQ Sequence 253 AA;

Query Match 60.4%; Score 400.5; DB 24; Length 253;  
 Best Local Similarity 63.2%; Pred. No. 2.3e-27;  
 Matches 79; Conservative 12; Mismatches 31; Indels 3; Gaps 1;  
 QY 2 VTDESGLGQTGGALSLVCKASGFTSSHGMMVVRQTPGKGLWVAGISNTGTYTYA 61  
 Db 2 VQLVESGGGLVQPGGSLRLCAASGFTSSYGMVVRQAPGKGLWVATISGGSYTYA 61  
 QY 62 PAVKGRATISRDNGQSTVRLQLNNLRADDTGYTCAGKAYCAGCGGIDDAWGHGTE 118  
 Db 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYICARRNVCSTGTCYSDGMDVWGQGT 121  
 QY 119 VTSS 123  
 Db 122 VTSS 126

RESULT 10  
 AM24101  
 ID AM24101 standard; Protein; 384 AA.  
 XX  
 AC AM24101;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX  
 DE Human EST encoded protein SEQ ID NO: 1626.  
 XX  
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-US02687.  
 XX  
 PR 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 DR WPI; 2001-476164/51.  
 DR N-PSDB; AAH98760.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -

XX PS Claim 20; Page 1102-1103; 1275pp; English.  
 XX CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a  
 CC protein of the invention.  
 XX XX  
 SQ Sequence 384 AA;

Query Match 60.2%; Score 399; DB 22; Length 384;  
 Best Local Similarity 61.4%; Pred. No. 5e-27;  
 Matches 81; Conservative 11; Mismatches 30; Indels 10; Gaps 2;  
 QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYTYA 61  
 Db 21 VQLVESGGGLVQPGGSLRLSCLAAAGFTFSSYAMSVVRQAPGKGLWVSGIGSGSSTYYA 80  
 QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYTCAGK-GAYCAGCGG-----DID 111  
 Db 81 DSVKGRFTISRDNSQNTLYLQMNLSRAEDTAVTYCAKSHPAYTYGSGSYSHYYTYGMD 140  
 QY 112 AMHGTEVTIVSS 123  
 Db 141 VMGQGTIVTVSS 152

RESULT 11  
 ABG60414  
 ID ABG60414 standard; Protein; 95 AA.  
 XX AC ABG60414;  
 XX DT 30-JUL-2002 (first entry)  
 DE Selective targeting peptide #89.  
 XX Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;  
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;  
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;  
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;  
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;  
 KW gene therapy.  
 XX OS Synthetic.  
 XX PN WO200220769-A1.  
 XX PD 14-MAR-2002.  
 XX PF 07-SEP-2001; 2001WO-US27692.  
 XX PR 08-SEP-2000; 2000US-231266P.  
 XX PR 17-JAN-2001; 2001US-0765101.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PI Arap W, Pasqualini R;  
 XX WI; 2002-415731/44.  
 XX Targeting peptides identified by phage display, useful for targeting  
 PT delivery to an organ or tissue, particularly for treating a disease,  
 PT e.g. cancer, inflammatory or autoimmune diseases, infections or  
 PT cardiovascular disease -  
 XX PS Claim 22; Page 73; 317pp; English.  
 XX CC The invention relates to an isolated peptide of 100 amino acids or less

CC in size useful for targeting delivery to an organ or tissue, particularly  
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory  
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral  
 CC infection, cardiovascular disease or degenerative disease. The peptide is  
 CC also useful for inducing apoptosis, particularly to a subject with  
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,  
 CC inflammation or macular degeneration. Furthermore, the peptide is useful  
 CC for diagnosing the diseases cited above. Targeting peptides of the  
 CC invention can also be used to deliver an agent to a foetus, by attaching  
 CC a peptide to the agent and administering the peptide to a pregnant  
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting  
 CC peptides of the invention.  
 XX XX  
 SQ Sequence 95 AA;

Query Match 59.7%; Score 395.5; DB 23; Length 95;  
 Best Local Similarity 87.8%; Pred. No. 2.2e-27;  
 Matches 79; Conservative 6; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 AVTLDESGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYTY 60  
 Db 7 AVTLDESGGGLQTPGGALSIVCKASGFTFSSYPMGVVRQAPGKGLWVAVISSGT-TWY 65  
 QY 61 APAVKGRATISRDNGQSTVRLQNLNRAED 90  
 Db 66 APAVKGRATISRDNGQSTVRLQNLNRAED 95

RESULT 12  
 ABR01534  
 ID ABR01534 standard; Protein; 221 AA.  
 XX AC ABR01534;  
 XX DT 16-APR-2003 (first entry)  
 DE Human anti-TIMP-1 antibody heavy chain #32.  
 XX Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;  
 KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;  
 KW variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;  
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;  
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.  
 XX OS Homo sapiens.  
 XX PN WO200286085-A2.  
 XX PD 31-OCT-2002.  
 XX PF 24-APR-2002; 2002WO-US12801.  
 XX PR 24-APR-2001; 2001US-285683P.  
 XX PA (FARB ) BAYER CORP.  
 XX PA (MORP-) MORPHOSYS AG.  
 XX PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;  
 XX WI; 2003-129114/12.  
 XX DR N-PSDB; ABZ74805.  
 XX New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1)  
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder  
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate  
 PT hypertrophy or lung cancer -  
 XX PS Claim 20; Page 170; 228pp; English.  
 CC The invention relates to a novel purified preparation of a human  
 CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)  
 CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of



XX Claim 1; Column 43; 162pp; English.  
 XX  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH8615 to AAH8626 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification  
 CC of the present invention.  
 XX  
 SQ Sequence 127 AA;

Query Match 59.3%; Score 393; DB 22; Length 127;  
 Best Local Similarity 61.9%; Pred. No. 5e-27;  
 Matches 78; Conservative 12; Mismatches 32; Indels 4; Gaps 1;  
 QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTTPGKGLWVAGISNTGTYTYA 61  
 Db 2 VQLLESGGGLVQPGGSLRLSCAASGFTFSSYSHWVRQAPGKGLWVSSISNSNTIYYA 61  
 QY 62 PAVKGRATISRDNQSTVRLQLNLRADTGTYYCAKGGAYCAGC---GGDIDAWGHGT 117  
 Db 62 DAVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARDSTRYSNFLRWVRSDGMDVWGOT 121  
 QY 118 EVIVSS 123  
 Db 122 TVIVSS 127

RESULT 15  
 ABR01513  
 ID ABR01513 standard; Protein; 224 AA.  
 AC ABR01513;  
 DT 16-APR-2003 (first entry)  
 XX Human anti-TIMP-1 antibody heavy chain #11.  
 DE  
 KW Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;  
 KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;  
 KW variable light chain; cytosolic; nephrotropic; cardiant; liver fibrosis;  
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;  
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200286085-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 24-APR-2002; 2002WO-US12801.  
 XX  
 PR 24-APR-2001; 2001US-285683P.  
 XX  
 PA (FARB ) BAYER CORP.  
 PA (MORP-) MORPHOSYS AG.  
 XX  
 PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;  
 XX  
 DR WPI; 2003-129114/12.  
 DR N-PSDB; AB274784.  
 XX  
 PT New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1)  
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder  
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate  
 PT hypertrophy or lung cancer

XX Claim 20; Page 155; 228pp; English.  
 XX  
 CC The invention relates to a novel purified preparation of a human  
 CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)  
 CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of  
 CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and  
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant  
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
 CC activity of a TIMP-1. It is especially useful for ameliorating the  
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic  
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon  
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
 CC chain regions of a human anti-TIMP-1 antibody of the invention.  
 XX  
 SQ Sequence 224 AA;

Query Match 59.2%; Score 392.5; DB 24; Length 224;  
 Best Local Similarity 64.8%; Pred. No. 1e-26;  
 Matches 79; Conservative 11; Mismatches 29; Indels 3; Gaps 1;  
 QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTTPGKGLWVAGISNTGTYTYA 61  
 Db 2 VQLLESGGGLVQPGGSLRLSCAASGFTFSSYSHWVRQAPGKGLWVSSISNSNTIYYA 61  
 QY 62 PAVKGRATISRDNQSTVRLQLNLRADTGTYYCAKGGAYCAGCGGDDAWGHGTEVIV 121  
 Db 62 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARYMAYMAEA---IDVWGQSTLVTV 118  
 QY 122 SS 123  
 Db 119 SS 120

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OM protein - protein search, using sw model

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Title: US-10-083-424A-18

Perfect score: 663

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

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Listing first 45 summaries

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- 4: /cgn2.6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2.6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	79.9	146	3	US-08-751-359-15
2	530	79.9	146	4	US-08-907-146-15
3	496.5	74.9	141	3	US-08-751-359-17
4	496.5	74.9	141	4	US-08-907-146-17
5	494.5	74.6	147	3	US-08-751-359-18
6	494.5	74.6	147	4	US-08-907-146-18
7	478.5	72.2	145	3	US-08-751-359-16
8	478.5	72.2	145	4	US-08-907-146-16
9	444	67.0	120	3	US-08-751-359-25
10	444	67.0	120	4	US-08-907-146-25
11	393	59.3	127	3	US-09-240-274-27
12	390.5	58.9	122	2	US-08-958-201-6
13	387.5	58.4	140	3	US-08-983-607-32
14	387	58.4	125	2	US-08-428-197-1
15	387	58.4	125	5	PCT-US93-10555-1
16	386.5	58.3	131	3	US-08-983-607-28
17	385.5	58.1	124	3	US-08-983-607-47
18	385	58.1	120	2	US-08-428-197-20
19	385	58.1	120	2	US-08-428-197-22
20	385	58.1	120	2	US-08-428-197-30
21	385	58.1	120	2	US-08-428-197-32
22	385	58.1	120	5	PCT-US93-10555-20
23	385	58.1	120	5	PCT-US93-10555-22
24	385	58.1	120	5	PCT-US93-10555-30
25	385	58.1	120	5	PCT-US93-10555-32
26	383.5	57.8	120	4	US-09-025-769B-38
27	383.5	57.8	120	4	US-09-025-769B-63

28	383.5	57.8	281	4	US-09-025-769B-178	Sequence 178, Appl
29	382	57.6	120	2	US-08-428-197-24	Sequence 24, Appl
30	382	57.6	120	2	US-08-428-197-26	Sequence 26, Appl
31	382	57.6	120	2	US-08-428-197-28	Sequence 28, Appl
32	382	57.6	120	2	US-08-428-197-40	Sequence 40, Appl
33	382	57.6	120	5	PCT-US93-10555-24	Sequence 24, Appl
34	382	57.6	120	5	PCT-US93-10555-26	Sequence 26, Appl
35	382	57.6	120	5	PCT-US93-10555-28	Sequence 28, Appl
36	382	57.6	120	5	PCT-US93-10555-40	Sequence 40, Appl
37	382	57.6	249	4	US-10-039-785-53	Sequence 53, Appl
38	381.5	57.5	245	4	US-08-918-148-78	Sequence 78, Appl
39	381	57.5	117	3	US-08-983-607-46	Sequence 46, Appl
40	381	57.5	117	3	US-09-157-370-1	Sequence 1, Appl
41	381	57.5	131	3	US-09-240-274-28	Sequence 28, Appl
42	380.5	57.4	116	3	US-08-983-607-36	Sequence 36, Appl
43	379	57.2	123	1	US-08-478-039-104	Sequence 104, App
44	379	57.2	123	1	US-08-476-349A-104	Sequence 104, App
45	379	57.2	123	4	US-09-560-198A-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-751-359-15  
; Sequence 15, Application US/08751359  
; Patent No. 6143559  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08751,359  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 510  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 146 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-751-359-15

Query Match 79.9%; Score 530; DB 3; Length 146;  
Best Local Similarity 82.7%; Pred. No. 2.8e-42;  
Matches 105; Conservative 2; Mismatches 16; Indels 4; Gaps 1;

QY 1 AVTLDESGGLQTPGGALSLVCKASGTFSSHGMWVROTCKGLWVAGISNTGTYTY 60  
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DB 20 AVTLDESGGLQTPGGALSLVCKASGTFSSHGMWVROAPGKGLFVAGIDNTGRYTY 79  
|||||

QY 61 APAVKGRATISRNGQSTVRLQLNNLRAEDTGYTCAKGGAYCAGCG---GDIDAWHG 116  
Db 80 GSAVKGRATISRNGQSTVRLQLNNLRAEDTGYTCAKAGSAYCGGAYTAGSIDAWHG 139  
QY 117 TEVIVSS 123  
Db 140 TEVIVSS 146

## RESULT 2

US-08-907-146-15  
; Sequence 15, Application US/08907146  
; Patent No. 6316600  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/907,146  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/751,359  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 146 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear

US-08-907-146-15

Query Match 79.9%; Score 530; DB 4; Length 146;  
Best Local Similarity 82.7%; Pred. No. 2.8e-42;  
Matches 105; Conservative 2; Mismatches 16; Indels 4; Gaps 1;  
QY 1 AVTLDSEGGGLQTPGGALSLVCKASGTFSSHGMWVRQTPGKGLWVAGISNTGYTY 60  
Db 20 AVTLDSEGGGLQTPGRALSLVCKASGTFSSYNGWVRQAPGKGLFVAGIDNTGYTY 79

QY 61 APAVKGRATISRNGQSTVRLQLNNLRAEDTGYTCAKGGAYCAGCG---GDIDAWHG 116  
Db 80 GSAVKGRATISRNGQSTVRLQLNNLRAEDTGYTCAKAGSAYCGGAYTAGSIDAWHG 139

QY 117 TEVIVSS 123  
Db 140 TEVIVSS 146

## RESULT 3

US-08-751-359-17

; Sequence 17, Application US/08751359  
; Patent No. 6143559  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/751,359  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 510  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 141 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear

; NAME/KEY: Protein  
; LOCATION: 1..2  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /note= "x = any amino acid"  
US-08-751-359-17

Query Match 74.9%; Score 496.5; DB 3; Length 141;  
Best Local Similarity 81.3%; Pred. No. 3.5e-39;  
Matches 100; Conservative 4; Mismatches 18; Indels 1; Gaps 1;  
QY 1 AVTLDSEGGGLQTPGGALSLVCKASGTFSSHGMWVRQTPGKGLWVAGISNTGYTY 60  
Db 20 AVTLDSEGGGLQTPGGALSLVCKASGTFSSNGWVRQAPGKGLVYAGISSSKYTYG 79

QY 61 APAVKGRATISRNGQSTVRLQLNNLRAEDTGYTCAKGGAYCAGCGGDIDAWHGTEVI 120  
Db 80 GSAVKGRATISRNGQSTVRLQLNNLRAEDTGYTCAKGRSGFTCVIS-XTWGHGTEVI 138  
QY 121 VSS 123  
Db 139 VSS 141

## RESULT 4

US-08-907-146-17  
; Sequence 17, Application US/08907146  
; Patent No. 6316600  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Arnold, White & Durkee  
;; STREET: P.O. Box 4433  
;; CITY: Houston  
;; STATE: Texas  
;; COUNTRY: USA  
;; ZIP: 77210

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/907,146  
;; FILING DATE:

;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/751,359

;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Highlander, Steven L  
;; REGISTRATION NUMBER: 37,642  
;; REFERENCE/DOCKET NUMBER: ARSB:504

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 512/418-3000

;; TELEFAX: 512/474-7577

;; INFORMATION FOR SEQ ID NO: 17:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 141 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: linear

;; FEATURE:

;; NAME/KEY: Protein

;; LOCATION: 1..2

;; OTHER INFORMATION: /product= "OTHER"

;; OTHER INFORMATION: /note= "x = any amino acid"

US-08-907-146-17  
Query Match 74.9%; Score 496.5; DB 4; Length 141;  
Best Local Similarity 81.3%; Pred. No. 3.5e-39;  
Matches 100; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 1 AVTLDESGGLQTPGGSLVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYY 60  
|||||  
Db 20 AVTLDESGGLQTPGGSLVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYY 79  
|||||

QY 61 APVAVKGRATISRDNQSTVRLQLNLRADTGTYYCAKGAYCAGCGGDDIDAWGHGTEVI 120  
|||||  
Db 80 GSAVAVKGRATISRDNQSTVRLQLNLRADTGTYYCAKGAYCAGCGGDDIDAWGHGTEVI 138  
|||||

QY 121 VSS 123  
|||  
Db 139 VSS 141  
|||

RESULT 5  
US-08-751-359-18  
; Sequence 18, Application US/08/751359  
; Patent No. 6143559  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA

;; ZIP: 77210  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/751,359  
;; FILING DATE: Concurrently Herewith  
;; CLASSIFICATION: 510  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Highlander, Steven L  
;; REGISTRATION NUMBER: 37,642  
;; REFERENCE/DOCKET NUMBER: ARSB:504  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 512/418-3000  
;; TELEFAX: 512/474-7577  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 147 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; US-08-751-359-18

Query Match 74.6%; Score 494.5; DB 3; Length 147;  
Best Local Similarity 78.9%; Pred. No. 5.6e-39;  
Matches 101; Conservative 5; Mismatches 17; Indels 5; Gaps 2;

QY 1 AVTLDESGGLQTPGGSLVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYY 60  
|||||  
Db 20 AVTLDESGGLQTPGGSLVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYY 79  
|||||

QY 61 APVAVKGRATISRDNQSTVRLQLNLRADTGTYYCAK--GGAYC---AGCGGDDIDAWGH 115  
|||||  
Db 80 APVAVKGRATISRDNQSTVRLQLNLRADTGTYYCAKAGSGYSSDATIAGSIDAWGH 139  
|||||

QY 116 GTEVIVSS 123  
|||||  
Db 140 GTEVIVSS 147  
|||||

RESULT 6  
US-08-907-146-18  
; Sequence 18, Application US/08907146  
; Patent No. 6316600  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/907,146  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/751,359  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-907-146-18

Query Match 74.6%; Score 494.5; DB 4; Length 147;  
Best Local Similarity 78.9%; Pred. No. 5.6e-39;  
Matches 101; Conservative 5; Mismatches 17; Indels 5; Gaps 2;

QY 1 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGYTYY 60  
Db 20 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGYTYY 79  
QY 61 APAVKGRATISRDNGQSTVRLQNLNLRADTGTYYCAK---GGAYC---ACCGGDDAWGH 115  
Db 80 APAVKGRATISRDNGQSTVRLQNLNLRADTGTYYCAKAGSGYCSDATIASIDAWGH 139  
QY 116 GTEVIVSS 123  
Db 140 GTEVIVSS 147

RESULT 7  
US-08-751-359-16  
; Sequence 16, Application US/08751359  
; Patent No. 6143559  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08751,359  
; FILING DATE: Concurrently Herewith.  
; CLASSIFICATION: 510  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 145 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-751-359-16

Query Match 72.2%; Score 478.5; DB 3; Length 145;  
Best Local Similarity 77.2%; Pred. No. 1.7e-37;  
Matches 98; Conservative 6; Mismatches 18; Indels 5; Gaps 2;

QY 1 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGYTYY 60  
Db 20 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGYTYY 78  
QY 61 APAVKGRATISRDNGQSTVRLQNLNLRADTGTYYCAK---GGAYCAGCGGDDAWGH 116  
Db 79 GAAVKGRATISRDNGQSTVRLQNLNLRADTGTYYCAKESGGSGTSSYAANIDAWGH 138  
QY 117 TEVIVSS 123  
Db 139 TEVIVSS 145

RESULT 8  
US-08-907-146-16  
; Sequence 16, Application US/08907146  
; Patent No. 6316600  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/907,146  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/751,359  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 145 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-907-146-16

Query Match 72.2%; Score 478.5; DB 4; Length 145;  
Best Local Similarity 77.2%; Pred. No. 1.7e-37;  
Matches 98; Conservative 6; Mismatches 18; Indels 5; Gaps 2;

QY 1 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGYTYY 60  
Db 20 AVTLDESGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKLEWVAGISNTGYTYY 78  
QY 61 APAVKGRATISRDNGQSTVRLQNLNLRADTGTYYCAK---GGAYCAGCGGDDAWGH 116  
Db 79 GAAVKGRATISRDNGQSTVRLQNLNLRADTGTYYCAKESGGSGTSSYAANIDAWGH 138

QY 117 TEVIVSS 123  
| | | | |  
Db 139 TEVIVSS 145

RESULT 9  
US-08-751-359-25  
; Sequence 25, Application US/08751359  
; Patent No. 6143559  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/751,359  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 510  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-751-359-25

Query Match 67.0%; Score 444; DB 3; Length 120;  
Best Local Similarity 88.8%; Pred. No. 2.2e-34;  
Matches 87; Conservative 2; Mismatches 9; Indels 0; Gaps 0;  
QY 1 AVTLDSEGGGLTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGYTY 60  
| | | | |  
Db 20 AVTLDSEGGGLTPGRALSLVCKASGFTFSSYNNMGWVRQAPGKGLFVAGIDNTGRYTY 79  
| | | | |  
QY 61 APVKGRTISRDNQGSVRLQLNLRAEDTGYTCAC 98  
| | | | |  
Db 80 GSAVKGRATISRDNQGSVRLQLNLRAEDTGYTCAC 117  
| | | | |

RESULT 10  
US-08-907-146-25  
; Sequence 25, Application US/08907146  
; Patent No. 6316600  
; GENERAL INFORMATION:  
; APPLICANT: Michael, Nancy M  
; APPLICANT: Accavitti, Marianne  
; APPLICANT: Thompson, Craig B  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/907,146  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/751,359  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-907-146-25

Query Match 67.0%; Score 444; DB 4; Length 120;  
Best Local Similarity 88.8%; Pred. No. 2.2e-34;  
Matches 87; Conservative 2; Mismatches 9; Indels 0; Gaps 0;  
QY 1 AVTLDSEGGGLTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGYTY 60  
| | | | |  
Db 20 AVTLDSEGGGLTPGRALSLVCKASGFTFSSYNNMGWVRQAPGKGLFVAGIDNTGRYTY 79  
| | | | |  
QY 61 APVKGRTISRDNQGSVRLQLNLRAEDTGYTCAC 98  
| | | | |  
Db 80 GSAVKGRATISRDNQGSVRLQLNLRAEDTGYTCAC 117  
| | | | |

RESULT 11  
US-09-240-274-27  
; Sequence 27, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain E011s  
US-09-240-274-27  
Query Match 59.3%; Score 393; DB 3; Length 127;  
Best Local Similarity 61.9%; Pred. No. 1.3e-29;

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Matches 78; Conservative 12; Mismatches 32; Indels 4; Gaps 1;
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGTYTYA 61
Db 2 VQLLESGGGLVKPGSLRLSCAASGFTFSSYSMHWVRQAPGKLEWSSISNTYTYA 61
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGC- ---GGDIDAWGHGT 117
Db 62 DAVKGRFTISRDNKNTLSLQMSLRAEDTAVYYCARDYSNLFRLVRSQGMVWGQGT 121
QY 118 EVIVSS 123
Db 122 TVIVSS 127

RESULT 12
US-08-958-201-6
; Sequence 6, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 26
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US-08-958-201-6
; Query Match 58.9%; Score 390.5; DB 2; Length 122;
; Best Local Similarity 63.1%; Pred. No. 2.2e-29;
; Matches 77; Conservative 11; Mismatches 33; Indels 1; Gaps 1;
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGTYTYA 61
Db 2 VNLRESGGGLVKPGSLRLSCAASGFTFSDYNSWIRQAPGKLEWVSAISGSGNTYTYA 61
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGDIDAWGHGTIV 121
Db 62 DSVKGRFTISRDNKNTLSLQMSLRAEDTALTYCVK-GARAARAGGYFDLWGRGTLTV 120
QY 122 SS 123
Db 121 SS 122

RESULT 13
US-08-983-607-32
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; Sequence 32, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fuses5 fusion phage construct
; CLONE: V86
; FEATURE:
; NAME/KEY: heavy chain and linker
;
US-08-983-607-32
; Query Match 58.4%; Score 387.5; DB 3; Length 140;
; Best Local Similarity 63.7%; Pred. No. 4.8e-29;
; Matches 79; Conservative 12; Mismatches 30; Indels 3; Gaps 2;
QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMWVRQTPGKLEWVAGISNTGTYTYA 61
Db 2 VQLVQSGGGLVQPGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVAISGSGTYTYA 61
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGTYYCAKGGAYCAGCGD- -IDAWGHGTIV 119
Db 62 DSVKGRFTISRDNKNTLSLQMSLRAEDTAVYYCARGWG-LRGEEDYYMDVWKGNTWV 120
QY 120 IVSS 123
Db 121 TVSS 124
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APPLICANT: SILVERMAN, GREGG J.

Search completed: September 3, 2003, 12:18:23  
Job time : 12.3177 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:10:30 ; Search time 22.849 Seconds  
(without alignments)  
739.130 Million cell updates/sec

Title: US-10-083-424A-18

Perfect score: 663

Sequence: 1 AVTLDESGGLQTPGGALSL.....AGCGGDIDAWGHGTEVVS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	663	100.0	123	15	US-10-083-424-18
2	508.5	76.7	124	15	US-10-083-424-20
3	494	74.5	127	15	US-10-083-424-38
4	468	70.6	125	15	US-10-083-424-24
5	460.5	69.5	124	15	US-10-083-424-22
6	403.5	60.9	124	15	US-10-040-244-16
7	393.5	59.3	127	11	US-09-848-798-27
8	392.5	59.2	239	11	US-09-880-748-2023
9	390.5	58.9	239	11	US-09-880-748-1105
10	389.5	58.7	239	11	US-09-880-748-2022
11	389.5	58.7	247	11	US-09-880-748-996
12	388.5	58.6	249	11	US-09-880-748-892
13	388.5	58.6	249	11	US-09-880-748-896
14	387.5	58.4	254	11	US-09-880-748-1701
15	387	58.4	248	11	US-09-880-748-913

16	385.5	58.1	118	15	US-10-001-934-39	Sequence 39, Appl
17	385	58.1	123	15	US-10-269-805-59	Sequence 59, Appl
18	384.5	58.0	128	10	US-09-840-459-77	Sequence 77, Appl
19	384.5	58.0	128	10	US-09-840-459-79	Sequence 79, Appl
20	384.5	58.0	254	11	US-09-880-748-1295	Sequence 1295, Ap
21	384	57.9	121	10	US-09-822-698A-3	Sequence 3, Appli
22	384	57.9	381	10	US-09-822-698A-5	Sequence 5, Appli
23	384	57.9	451	10	US-09-822-698A-26	Sequence 26, Appl
24	383.5	57.8	120	14	US-10-025-687-4	Sequence 4, Appli
25	383.5	57.8	120	15	US-10-135-687-4	Sequence 4, Appli
26	383.5	57.8	239	11	US-09-880-748-1922	Sequence 1922, Ap
27	383	57.8	121	10	US-09-840-459-92	Sequence 92, Appl
28	382.5	57.7	124	10	US-09-840-459-89	Sequence 89, Appl
29	382.5	57.7	240	9	US-09-192-854-2	Sequence 2, Appli
30	382.5	57.7	240	10	US-09-968-561A-2	Sequence 2, Appli
31	382.5	57.7	240	12	US-09-968-744A-2	Sequence 2, Appli
32	382	57.6	123	10	US-09-840-459-82	Sequence 82, Appl
33	382	57.6	249	13	US-10-039-785-53	Sequence 53, Appl
34	382	57.6	254	11	US-09-880-748-1139	Sequence 1139, Ap
35	381.5	57.5	249	11	US-09-880-748-512	Sequence 512, App
36	381.5	57.5	249	11	US-09-880-748-1111	Sequence 1111, Ap
37	381	57.5	131	11	US-09-848-798-28	Sequence 28, Appl
38	381	57.5	248	11	US-09-880-748-1876	Sequence 1876, Ap
39	380.5	57.4	223	11	US-09-972-656-86	Sequence 86, Appl
40	380.5	57.4	243	11	US-09-880-748-1935	Sequence 1935, Ap
41	380.5	57.4	249	11	US-09-880-748-397	Sequence 397, App
42	380.5	57.4	249	11	US-09-880-748-911	Sequence 911, App
43	380.5	57.4	249	11	US-09-880-748-1102	Sequence 1102, Ap
44	380.5	57.4	249	11	US-09-880-748-1113	Sequence 1113, Ap
45	380.5	57.4	249	11	US-09-880-748-1115	Sequence 1115, Ap

## ALIGNMENTS

RESULT 1  
US-10-083-424-18  
; Sequence 18, Application US/10083424  
; Publication No. US20030104497A1  
; GENERAL INFORMATION:  
; APPLICANT: Avicore Biotechnology Institute Inc.  
; TITLE OF INVENTION: Recombinant SCFV Antibodies Specific to Eimeria spp. Respon  
; TITLE OF INVENTION: for Coccidiosis  
; FILE REFERENCE: Avicore-USA-1  
; CURRENT APPLICATION NUMBER: US/10/083.424  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: KR 2001-52934  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 18  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: chicken hybridoma cell line 2-1  
US-10-083-424-18

Query Match	100.0%	Score 663;	DB 15;	Length 123;
Best Local Similarity	100.0%;	Pred. No. 7.6e-53;		
Matches 123;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AVTLDESGGLQTPGGALSLVKASGFTFSSHGMMVVRQTPCKGLEWVAGISNTGTYTY 60		
Db	1	AVTLDESGGLQTPGGALSLVKASGFTFSSHGMMVVRQTPCKGLEWVAGISNTGTYTY 60		
QY	61	APAVKGRATISRDNGQSTVRLQLNLRADTGTYTCAGGAYCAGCGGDIDAWGHGTEVI 120		
Db	61	APAVKGRATISRDNGQSTVRLQLNLRADTGTYTCAGGAYCAGCGGDIDAWGHGTEVI 120		
QY	121	VSS 123		
Db	121	VSS 123		

RESULT 4			
US-10-083-424-24			
; Sequence 24, Application US/10083424			
; Publication No. US20030104497A1			
; GENERAL INFORMATION:			
; APPLICANT: Avicore Biotechnology Institute Inc.			
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Eimeria spp. Respons			
; TITLE OF INVENTION: for Coccidiosis			
; FILE REFERENCE: Avicore-USA-1			
; CURRENT APPLICATION NUMBER: US/10/083,424			
; PRIOR FILING DATE: 2002-02-19			
; PRIOR APPLICATION NUMBER: KR 2001-52934			
; PRIOR FILING DATE: 2001-08-30			
; NUMBER OF SEQ ID NOS: 40			
; SOFTWARE: KopatentIn 1.71			
; SEQ ID NO 24			
; LENGTH: 125			
; TYPE: PRT			
; ORGANISM: chicken hybridoma cell line 8C3			
US-10-083-424-24			
Query Match		70.6%; Score 468; DB 15; Length 125;	
Best Local Similarity		72.9%; Pred. No. 3.3e-35;	
Matches		94; Conservative 8; Mismatches 17; Indels 10; Gaps 2;	
QY	1	AVTLDESGGGLQTPGGALSIVCKASGFTTSSHGMMVROT	PGKGLEWVAGISNTGTYYT 60
DB	1	AVTLDESGGGLQTPGGGLSLVCKASGFSIGGYIMHVROT	PGKGLFVAGIDAGGGSTYY 60
QY	61	YAPAVKGRATISRDNGQSTVRLQNLNLRADTGTYYCAK	GAYCAGCGD-----IDAWG 114
DB	61	GAAVOGRAFVSRDNGQSTLRQLNLRLEDTGTFCAK	-----ASRCGYDWCADNIDAWG 116
QY	115	HGTEVIVSS	123
DB	117	HGTEVIVSS	125
RESULT 5			
US-10-083-424-22			
; Sequence 22, Application US/10083424			
; Publication No. US20030104497A1			
; GENERAL INFORMATION:			
; APPLICANT: Avicore Biotechnology Institute Inc.			
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Eimeria spp. Respons			
; TITLE OF INVENTION: for Coccidiosis			
; FILE REFERENCE: Avicore-USA-1			
; CURRENT APPLICATION NUMBER: US/10/083,424			
; PRIOR FILING DATE: 2002-02-19			
; PRIOR APPLICATION NUMBER: KR 2001-52934			
; PRIOR FILING DATE: 2001-08-30			
; NUMBER OF SEQ ID NOS: 40			
; SOFTWARE: KopatentIn 1.71			
; SEQ ID NO 22			
; LENGTH: 124			
; TYPE: PRT			
; ORGANISM: chicken hybridoma cell line 13C8			
US-10-083-424-22			
Query Match		69.5%; Score 460.5; DB 15; Length 124;	
Best Local Similarity		75.0%; Pred. No. 1.6e-34;	
Matches		93; Conservative 7; Mismatches 23; Indels 1; Gaps 1;	
QY	1	AVTLDESGGGLQTPGGALSIVCKASGFTTSSHGMMVROT	PGKGLEWVAGI-SNTGTYYT 59
DB	1	AVTLDESGGGLQTPGGGLSLVCKGSLDFFSYAMGWVQAP	PGKGLFVAGIKKNDGSMWN 60
QY	60	YAPAVKGRATISRDNGQSTVRLQNLNLRADTGTYYCAK	GAYCAGCGGDDIDAWGHGTEV 119
DB	61	YAPAVOGRAFVSRDNGQSTVRLQNLNLRADTGLIYVCT	RDNVNSGYDDAIDAWGHGTEV 120



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QY 120 IVSS 123
Db 121 IVSS 124

RESULT 6
US-10-040-244-16
; Sequence 16, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; PRIOR FILING DATE: 2002-06-17
; PRIOR FILING DATE: 2000-4-28
; PRIOR FILING DATE: 2001-04-27
; PRIOR FILING DATE: 2001-04-27
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 16
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-244-16

Query Match 60.9%; Score 403.5; DB 15; Length 124;
Best Local Similarity 65.9%; Pred. No. 2.2e-29;
Matches 81; Conservative 11; Mismatches 30; Indels 1; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYTYA 61
Db 2 VQLLESGGGLVPGGSLRLSCAASGFTFSSYAMSVVRQAPGKGLWVSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNQGSTVRLQLNLRADTGTYYCAKGGAYCAGCGDIDAMGHGTEVI 120
Db 62 DSVKGRFTISRDNKNTLYLQMSLRADTAVYYCAKDGYYGSGSYGYFDYWGQGLT 121

QY 121 VSS 123
Db 122 VSS 124

RESULT 7
US-09-848-798-27
; Sequence 27, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain E01is
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US-09-848-798-27

Query Match 59.3%; Score 393; DB 11; Length 127;
Best Local Similarity 61.9%; Pred. No. 2e-28;
Matches 78; Conservative 12; Mismatches 32; Indels 4; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYTYA 61
Db 2 VQLLESGGGLVPGGSLRLSCAASGFTFSSYAMSVVRQAPGKGLWVSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNQGSTVRLQLNLRADTGTYYCAKGGAYCAGCGDIDAMGHGCT 117
Db 62 DAVKGRFTISRDNKNSLYLQMSLRADTAVYYCARDSTRYFLRWVRSDGMVWGOST 121

QY 118 EVIVSS 123
Db 122 TVIVSS 127

RESULT 8
US-09-880-748-2023
; Sequence 2023, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2023
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2023

Query Match 59.2%; Score 392.5; DB 11; Length 239;
Best Local Similarity 62.3%; Pred. No. 4.4e-28;
Matches 76; Conservative 13; Mismatches 26; Indels 7; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSIVCKASGFTFSSHGMMVVRQTPGKGLWVAGISNTGTYTYA 61
Db 2 VQLQESGGVVPQGGSLRLSCAASGFTFSGYGMHVRQAPGKGLWVSAISGSGSTYYA 61

QY 62 PAVKGRATISRDNQGSTVRLQLNLRADTGTYYCAKGGAYCAGCGDIDAMGHGTEVI 121
Db 62 DSVKGRFTISRDNKNSLYLQMSLRADTAVYYCARGDAY-----FDYWGQGTMTVTV 114

QY 122 SS 123
Db 115 SS 116

RESULT 9
US-09-880-748-1105
; Sequence 1105, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
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; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 892
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-892

Query Match
  Best Local Similarity 58.6%; Score 388.5; DB 11; Length 249;
Matches 80; Conservative 10; Mismatches 32; Indels 3; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTPGKLEWVAGISNTGTYTYA 61
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Db 2 VHLRESGGGLVQPGSLRLSCAASGFTFSSYGMHWVROAPGKLEWVAVISYDGSNKYYA 61
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QY 62 PAVKGRATISRDNGQSTVRLQNLNLRADTGYTCAGKAYCAGCGD---IDANGHGT 118
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Db 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDGYDILTGYSYGMDVWGQGL 121
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QY 119 VIVSS 123
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Db 122 VTVSS 126

RESULT 13
US-09-880-748-896
; Sequence 896, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 896
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-896

Query Match
  Best Local Similarity 58.6%; Score 388.5; DB 11; Length 249;
Matches 79; Conservative 11; Mismatches 32; Indels 3; Gaps 1;

QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTPGKLEWVAGISNTGTYTYA 61
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Db 2 VNLRESGGVQVQGRSLRLSCAASGFTFSSYGMHWVROAPGKLEWVAGISYDGSNKYYA 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 62 PAVKGRATISRDNGQSTVRLQNLNLRADTGYTCAGKAYCAGCGD---IDANGHGT 118
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 HSKVGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDGYDILTGYSYGMDVWGQGT 121
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QY 119 VIVSS 123
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Db 122 VTVSS 126

RESULT 14
US-09-880-748-1701
; Sequence 1701, Application US/09880748
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1701
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1701

Query Match
  Best Local Similarity 58.4%; Score 387.5; DB 11; Length 254;
Matches 78; Conservative 11; Mismatches 33; Indels 5; Gaps 1;
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QY 2 VTLDSEGGGLQTPGGALSLVCKASGFTFSSHGMMVROTPGKLEWVAGISNTGTYTYA 61
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Db 2 VOLQESGGGLVKPGGSLRLSCAASGFTFSSYAMSVROAPGKLEWVSAISGSGSTYYA 61
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 62 PAVKGRATISRDNGQSTVRLQNLNLRADTGYTCAGKAYCAGCGG-----DIDAWGHG 116
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDGYDILTGYHYGMDVWGGRG 121
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QY 117 TEVIVSS 123
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Db 122 TMVTVSS 128
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RESULT 15
US-09-880-748-913
; Sequence 913, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 913
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-913

Query Match
  Best Local Similarity 58.4%; Score 387; DB 11; Length 248;
Matches 78; Conservative 12; Mismatches 27; Indels 10; Gaps 2;
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Db 2 VQLVESGGGLVQPGSLRLSCAAGFTFSSYMNWVRQAPKGLEWYSSISNRGSYIYA 61  
QY 62 PAVKGRATISRDNGQSTVRLQNLNRAEDTGYCAK-----GGAYCAGCGGDEDAWGH 115  
Db 62 DSVKGRFTISRDNAKNTLYLQMNLSRAEDTAVYYCAREGRDILTGVYYG----LDVWGO 117  
QY 116 GTEVIYSS 123  
Db 118 GTLVTYSS 125

Search completed: September 3, 2003, 12:53:14  
Job time : 23.849 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 12:09:30 ; Search time 198.914 Seconds  
(without alignments)  
538.192 Million cell updates/sec

Title: US-10-083-424A-18

Perfect score: 663

Sequence: 1 AVTLDESGGLQTPGGALSL.....AGCGGDIDAWGHGTEIVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main.\*  
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31: /cgn2\_6/ptodata/1/paa/US109\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	663	100.0	123	26	US-10-083-424-18
2	663	100.0	123	26	US-10-083-424A-18

Sequence 18, Appl  
Sequence 18, Appl

3	541	81.6	585	22	US-09-791-537-4487	Sequence 4487, Ap
4	541	81.6	585	22	US-09-791-537-63314	Sequence 63314, A
5	538	81.1	250	22	US-09-791-537-130345	Sequence 130345, A
6	537	81.0	236	22	US-09-791-537-129947	Sequence 129947, A
7	534	80.5	235	22	US-09-791-537-129977	Sequence 129977, A
8	534	80.5	237	22	US-09-791-537-129974	Sequence 129974, A
9	534	80.5	248	22	US-09-791-537-130354	Sequence 130354, A
10	527	79.5	242	22	US-09-791-537-130363	Sequence 130363, A
11	525	79.2	245	22	US-09-791-537-139118	Sequence 139118, A
12	524.5	79.1	258	1	PCT-US02-29003A-55	Sequence 55, Appl
13	524.5	79.1	258	1	PCT-US02-29003B-55	Sequence 55, Appl
14	522	78.7	138	22	US-09-791-537-44408	Sequence 44408, A
15	521.5	78.7	234	22	US-09-791-537-129944	Sequence 129944, A
16	521	78.6	124	22	US-09-791-537-129879	Sequence 129879, A
17	519.5	78.4	123	22	US-09-791-537-129857	Sequence 129857, A
18	519	78.3	234	22	US-09-791-537-133373	Sequence 133373, A
19	516.5	77.9	126	22	US-09-791-537-68235	Sequence 68235, A
20	515.5	77.8	122	22	US-09-791-537-129900	Sequence 129900, A
21	515	77.7	246	22	US-09-791-537-130347	Sequence 130347, A
22	515	77.7	252	1	PCT-US02-29003A-58	Sequence 58, Appl
23	515	77.7	252	1	PCT-US02-29003B-58	Sequence 58, Appl
24	513	77.4	250	1	PCT-US02-29003A-60	Sequence 60, Appl
25	513	77.4	250	1	PCT-US02-29003B-60	Sequence 60, Appl
26	510	76.9	231	22	US-09-791-537-135106	Sequence 135106, A
27	510	76.9	244	22	US-09-791-537-130346	Sequence 130346, A
28	510	76.9	244	22	US-09-791-537-130378	Sequence 130378, A
29	509	76.8	121	22	US-09-791-537-129880	Sequence 129880, A
30	508.5	76.7	124	26	US-10-083-424A-20	Sequence 20, Appl
31	508.5	76.7	124	26	US-10-083-424A-20	Sequence 20, Appl
32	506.5	76.4	233	22	US-09-791-537-129946	Sequence 129946, A
33	506	76.3	234	22	US-09-791-537-130343	Sequence 130343, A
34	505.5	76.2	124	22	US-09-791-537-129918	Sequence 129918, A
35	503	75.9	244	22	US-09-791-537-130380	Sequence 130380, A
36	503	75.7	131	22	US-09-791-537-71539	Sequence 71539, A
37	501.5	75.6	254	1	PCT-US02-29003A-56	Sequence 56, Appl
38	501.5	75.6	254	1	PCT-US02-29003B-56	Sequence 56, Appl
39	500.5	75.5	120	22	US-09-791-537-71513	Sequence 71513, A
40	500.5	75.5	128	22	US-09-791-537-68204	Sequence 68204, A
41	500.5	75.5	132	22	US-09-791-537-68219	Sequence 68219, A
42	500.5	75.5	250	1	PCT-US02-29003A-54	Sequence 54, Appl
43	500.5	75.5	250	1	PCT-US02-29003A-62	Sequence 62, Appl
44	500.5	75.5	250	1	PCT-US02-29003B-54	Sequence 54, Appl
45	500.5	75.5	250	1	PCT-US02-29003B-62	Sequence 62, Appl

#### ALIGNMENTS

RESULT 1  
US-10-083-424-18  
; Sequence 18, Application US/10083424  
; GENERAL INFORMATION:  
; APPLICANT: Avicore Biotechnology Institute Inc.  
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Eimeria spp. Response  
; FILE REFERENCE: Avicore-USA-1  
; TITLE OF INVENTION: for Coccidiosis  
; FILE REFERENCE: Avicore-USA-1  
; CURRENT APPLICATION NUMBER: US/10/083,424  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: KR 2001-52934  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 18  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: chicken hybridoma cell line 2-1  
US-10-083-424-18

Query Match 100.0%; Score 663; DB 26; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.7e-56;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTSSHHMMVVRQTPGKLEWAGISNIGTGYTY 60

Db 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60  
61 APVKGGRATISRDNQSTVRLQNLNLRADTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120  
61 APVKGGRATISRDNQSTVRLQNLNLRADTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120  
121 VSS 123  
121 VSS 123  
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RESULT 2  
US-10-083-424A-18  
; Sequence 18, Application US/10083424A  
; GENERAL INFORMATION:  
; APPLICANT: Avicore Biotechnology Institute Inc.  
; TITLE OF INVENTION: Recombinant ScFv Antibodies Specific to Eimeria spp. Responsible  
; FILE REFERENCE: for Coccidiosis  
; CURRENT APPLICATION NUMBER: US/10/083.424A  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: KR 2001-52934  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 18  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: chicken hybridoma cell line 2-1  
US-10-083-424A-18

Query Match 100.0%; Score 663; DB 26; Length 123;  
Best Local Similarity 100.0%; Pred. No. 2.7e-56;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60  
Db 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60  
QY 61 APVKGGRATISRDNQSTVRLQNLNLRADTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120  
Db 61 APVKGGRATISRDNQSTVRLQNLNLRADTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120  
QY 121 VSS 123  
Db 121 VSS 123

RESULT 3  
US-09-791-537-4487  
; Sequence 4487, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791.537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4487  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-791-537-4487

Query Match 81.6%; Score 541; DB 22; Length 585;  
Best Local Similarity 82.9%; Pred. No. 1.2e-43;  
Matches 102; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60  
Db 20 AVTLDESGGLQTPGGALSLVCKASGFTFSSYSGMMRQAPGKGLEWAGIDDDGSGTGY 79  
QY 61 APVKGGRATISRDNQSTVRLQNLNLRADTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120  
Db 80 GPAVQGRATISRDNQSTVRLQNLNLRADTGTYYCAKGGAYCAGCGGIDAWHGTEVI 139  
QY 121 VSS 123  
Db 140 VSS 142

RESULT 4  
US-09-791-537-63314  
; Sequence 63314, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791.537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 63314  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-791-537-63314

Query Match 81.6%; Score 541; DB 22; Length 585;  
Best Local Similarity 82.9%; Pred. No. 1.2e-43;  
Matches 102; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVVRQTPGKGLEWAGISNTGTYTY 60  
Db 20 AVTLDESGGLQTPGGALSLVCKASGFTFSSYSGMMRQAPGKGLEWAGIDDDGSGTGY 79  
QY 61 APVKGGRATISRDNQSTVRLQNLNLRADTGTYYCAKGGAYCAGCGGIDAWHGTEVI 120  
Db 80 GPAVQGRATISRDNQSTVRLQNLNLRADTGTYYCAKGGAYCAGCGGIDAWHGTEVI 139  
QY 121 VSS 123  
Db 140 VSS 142

RESULT 5  
US-09-791-537-130345  
; Sequence 130345, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791.537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 130345  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-791-537-130345

Query Match 81.1%; Score 538; DB 22; Length 250;  
Best Local Similarity 83.5%; Pred. No. 9.2e-44;  
Matches 106; Conservative 3; Mismatches 14; Indels 4; Gaps 2;

Query Match 80.5%; Score 534; DB 22; Length 248;

Best Local Similarity 82.7%; Pred. No. 2.2e-43;  
Matches 105; Conservative 3; Mismatches 15; Indels 4; Gaps 2;  
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVROTPPGKLEWVAGISNTGTYTY 60  
Db 122 AVTLDESGGLQTPGGTSLVCKASGFTFSSFNFWROAPGKLEWVGQITYSGRYTSY 181  
QY 61 APAVKGRATISRDNQSTVRLQNLNRAEDTGYTCAGG-AYC---AGCGGDIDAWGHG 116  
Db 182 APAVKGRATISRDNQSTVRLQNLNRAEDTATYYCAKGSYCNTRGCGVGTIDAWGHG 241  
QY 117 TEVIVSS 123  
Db 242 TEVIVSS 248

RESULT 10  
US-09-791-537-130363  
; Sequence 130363, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 130363  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-791-537-130363

Query Match 79.5%; Score 527; DB 22; Length 242;  
Best Local Similarity 82.8%; Pred. No. 1e-42;  
Matches 106; Conservative 2; Mismatches 10; Indels 10; Gaps 2;  
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVROTPPGKLEWVAGISNTGTYTY 60  
Db 120 AVTLDESGGLQTPGGALSLVCKASGFTFSSYGMQWVROAPGKLELIASISKTGYTY 179  
QY 61 APAVKGRATISRDNQSTVRLQNLNRAEDTGYTCAGGAYCAGCG-----GDIDAWGH 115  
Db 180 GSAVKGRATISRDNQSTVRLQNLNRAEDTGYTCAK-----ACGYSYETGCDIDAWGH 234  
QY 116 TEVIVSS 123  
Db 235 TEVIVSS 242

RESULT 11  
US-09-791-537-139118  
; Sequence 139118, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 139118  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-791-537-139118

Query Match 79.2%; Score 525; DB 22; Length 245;  
Best Local Similarity 82.5%; Pred. No. 1.7e-42;  
Matches 104; Conservative 6; Mismatches 10; Indels 6; Gaps 2;  
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVROTPPGKLEWVAGISNTGTYTY 60  
Db 123 AVTLDESGGLQTPGGALSLVCKASGFTFSSYGMQWVROAPGKLEVVASISKTGYTY 182  
QY 61 APAVKGRATISRDNQSTVRLQNLNRAEDTGYTCYCAK---GGAYCAGCGDDIDAWGHGT 117  
Db 183 GSAVKGRATISRDNQSTVRLQNLNRAEDTGSYYCAKPGACGHSYDSC---LDANGHGT 239  
QY 118 EVIVSS 123  
Db 240 EVIVSS 245

RESULT 12  
PCT-US02-29003A-55  
; Sequence 55, Application PC/TUS0229003A  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten  
; APPLICANT: Forschung e.V.  
; APPLICANT: ZHANG, Mei Yun  
; APPLICANT: SCHILLBERG, Stefan  
; APPLICANT: ZIMMERMANN, Sabine  
; APPLICANT: DI FIORE, Stefano  
; APPLICANT: EMANS, Neil  
; APPLICANT: FISCHER, Rainer  
; TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Met  
; TITLE OF INVENTION: of Making and Using  
; FILE REFERENCE: FRAU-202.1PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/29003A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/318,904  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: ScFv P6  
PCT-US02-29003A-55

Query Match 79.1%; Score 524.5; DB 1; Length 258;  
Best Local Similarity 82.0%; Pred. No. 2e-42; Mismatches 2; Indels 5; Gaps 3;  
Matches 105; Conservative 2; Mismatches 2; Indels 5; Gaps 3;  
QY 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSHGMMVROTPPGKLEWVAGISNTGTYTY 60  
Db 1 AVTLDESGGLQTPGGALSLVCKASGFTFSSYGMQWVROAPGKLEWVAGIDAGIYTY 60  
QY 61 APAVKGRATISRDNQSTVRLQNLNRAEDTGYTCAGG-AYC---ACGGD-IDAWGH 115  
Db 61 GAAVKGRATISRDNQSTVRLQNLNRAEDTGYTCAGGAYCDSGTWCADDYIDAWGH 120  
QY 116 TEVIVSS 123  
Db 121 TEVIVSS 128

RESULT 13  
PCT-US02-29003B-55  
; Sequence 55, Application PC/TUS0229003B  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten  
; APPLICANT: Forschung e.V.  
; APPLICANT: ZHANG, Mei Yun  
; APPLICANT: SCHILLBERG, Stefan  
; APPLICANT: ZIMMERMANN, Sabine  
; APPLICANT: DI FIORE, Stefano



Query Match	78.7%;	Score 522;	DB 22;	Length 138;
Best Local Similarity	84.6%;	Pred. No. 1.7e-42;		
Matches 104;	Conservative 2;	Mismatches 13;	Indels 4;	Gaps 1;

  

QY	1	AVTLDESGGLOTPGCGALSIVCKASGFTFSHGMMWVROTPGKGLEWVAGISNCTGTTYY	60
Db			
	20	AVTLDESGGLOTPGCGALSIVCKASGFTFSYNGWVROQAPGKGLEWVAGIDNTRGTGY	79
QY	61	APAVKGRATISRDNGOSTVRLQNLNRAEDTGYYCAKGCAYGACGGCGDIDAMGHGTEVI	120
Db			
	80	GSVAKGRATISRDNGOSTVRLQNLNRAEDTGYYCAK-----AAGTAGSIDAMGHGTEVI	135
QY	121	VSS	123
Db	136	VSS	138

Search completed: September 3, 2003, 12:49:33  
Job time : 200.014 secs

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